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96391

From: Kaushal, Sumesh
Sent: Wednesday, June 11, 2003 2:59 PM
To: STIC-Biotech/ChemLib
Subject: 09/663542: SEQ search

09/663542: SEQ search

Title: PHOSPHODIESTERASE ENZYMES
Inventor: FIDOCK, MARK

Please search

SEQ ID NO:1
SEQ ID NO:1 1-194

SEQ ID NO:2

priority : 01/21/00

thanks

S. Kaushal

CM1 12A07 AU1636

Ph: 703-305-6838

Mail Box: 11E12

CRFE

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 6/13/03
Date Completed: 6/23/03
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Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: 2
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: 01/02
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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File: 09663542

☒ IDS

☒ SEQ Search -- Interference Search Removed ☒ 6/28/03

☒ Search Report -- In file []

[] Reference Cited

Notes:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:46:07 ; Search time 5.52392 seconds
(without alignments)
1033.333 Million cell updates/sec

Title: US-09-663-542-1-copy_1_194

Perfect score: 975

Sequence: 1 MLKQARRPLFRNLSATQWK.....VLLLEDIESPVVKFTKSFEL 194

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307.5	31.5	875	1 US-08-480-547A-10	Sequence 10, Appl
2	307.5	31.5	875	1 US-08-480-547A-23	Sequence 23, Appl
3	307.5	31.5	875	1 US-08-250-847B-10	Sequence 10, Appl
4	307.5	31.5	875	1 US-08-250-847B-23	Sequence 23, Appl
5	307.5	31.5	875	2 US-08-463-949A-10	Sequence 10, Appl
6	307.5	31.5	875	2 US-08-463-949A-23	Sequence 23, Appl
7	307.5	31.5	875	3 US-08-464-410A-10	Sequence 10, Appl
8	307.5	31.5	875	3 US-08-464-410A-23	Sequence 23, Appl
9	307.5	31.5	875	3 US-09-226-741-5	Sequence 5, Appl
10	307.5	31.5	875	4 US-09-595-514-5	Sequence 5, Appl
11	307.5	31.5	875	5 PCT-US94-06066-23	Sequence 23, Appl
12	307.5	30.9	875	5 PCT-US94-06066-10	Sequence 10, Appl
13	186	19.1	367	4 US-09-226-741-3	Sequence 3, Appl
14	186	19.1	367	4 US-09-595-514-3	Sequence 3, Appl
15	186	19.1	490	3 US-09-226-741-1	Sequence 1, Appl
16	186	19.1	490	4 US-09-595-514-1	Sequence 1, Appl
17	165	16.9	766	2 US-08-951-648-2	Sequence 2, Appl
18	165	16.9	766	2 US-09-174-437-2	Sequence 2, Appl
19	165	16.9	779	2 US-08-951-648-6	Sequence 6, Appl
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21	165	16.9	803	2 US-08-951-648-4	Sequence 4, Appl
22	165	16.9	803	4 US-09-174-437-4	Sequence 4, Appl
23	162	16.6	905	4 US-09-754-250-4	Sequence 4, Appl
24	162	16.6	920	4 US-07-754-250-2	Sequence 2, Appl
25	162	16.6	941	1 US-07-872-644-45	Sequence 45, Appl
26	162	16.6	941	1 US-08-297-494-45	Sequence 45, Appl
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28	162	16.6	941	1 US-08-479-532-45	Sequence 45, Appl
29	162	16.6	941	1 US-08-455-526-45	Sequence 45, Appl
30	162	16.6	941	1 US-08-455-525-45	Sequence 45, Appl
31	162	16.6	941	3 US-09-139-491-45	Sequence 45, Appl
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34	154	15.8	921	1 US-08-297-494-39	Sequence 39, Appl
35	154	15.8	921	1 US-08-297-510-39	Sequence 39, Appl
36	154	15.8	921	1 US-08-479-532-39	Sequence 39, Appl
37	154	15.8	921	1 US-08-455-526-39	Sequence 39, Appl
38	154	15.8	921	1 US-08-455-525-39	Sequence 39, Appl
39	154	15.8	921	3 US-09-139-491-39	Sequence 39, Appl
40	154	15.8	921	4 US-09-754-250-5	Sequence 5, Appl
41	154	15.8	921	5 PCT-US92-03222-39	Sequence 39, Appl
42	154	15.8	942	1 US-07-872-644-43	Sequence 43, Appl
43	154	15.8	942	1 US-08-297-494-43	Sequence 43, Appl
44	154	15.8	942	1 US-08-297-510-43	Sequence 43, Appl
45	154	15.8	942	1 US-08-479-532-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-480-547A-10
; Sequence 10, Application US/08480547A
; Patent No. 5652131
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlec, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,547A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565213land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32791
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-547A-10

Query Match 31.5% Score 307.5; DB 1; Length 875;

APPLICANT: Ferguson, Kenneth M.
 APPLICANT: Francis, Sharon H.
 APPLICANT: Kadlecak, Ann
 APPLICANT: Loughney, Kate
 APPLICANT: McAllister-Lucas, Linda M.
 APPLICANT: Sonnenburg, William K.
 APPLICANT: Thomas, Melissa K.
 TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
 TITLE OF INVENTION: Phosphodiesterase Materials and Methods
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,410A
 FILING DATE: June 5, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6037119aud, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/32705
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 875 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-464-410A-10

237 EDPRFAEVDPDITGYKTSILCMPINKHREEVWGVAQAINKSGNGGTFTEKDEKDFAY 299

113 LPFGCISNAQLFAASRKEYERSKALLLEVNDLFEEQTDLEKIVKTMHRAQTLLKCR 172

297 LAFCGIVLHNAQLYETSILENKRQNVILDIASLIFEEOQSLEVLKKTAAITIISPMQVK 356

173 CSVLLED 180

357 CTIFIVDE 364

RESULT 8
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; Sequence 23: Application US/08464410A
; Patent No. 6037119
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecsek, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.

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RESULT 9
US-09-226-741-5
; Sequence 5, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 5
; LENGTH: 875
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: GI 3355606

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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 875
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: GI 3355606
US-09-595-514-5

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Best Local Similarity 46.18;   Pred. No. 3.1e-26;
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Db      247  EDPFNAEVDQITGYKTQSILCMPIKHNREEVGVGAINKKSGNGTFTTEKDEKFAAY 306.
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QY      113  LPFCGIAISNAQLFAASRKVEYSRALLEVNDLFEETOLEKTVKIMHRAQTLTKKER 172
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Db      307  LAFCGIVLHNAQLYETSLLENKRNQVLLDLASLIFEQQSLEVLKXIAATISFMQVQK 366
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QY      173  CSVLLED 180
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Db      367  CTIFIVDE 374

RESULT 11
PCT-US94-060666-23
; Sequence 23, Application PC/TUS9406066
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Washington
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,051
; FILING DATE: 27-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-06066-10

Query Match          30.9%; Score 301.5; DB 5; Length 875;
Best Local Similarity 45.3%; Pred. No. 1.5e-25;
Matches 59; Conservative 32; Mismatches 37; Indels 1; Gaps 1;

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Qy      113  LPFCGTASNAQLFAASRKEVEYSRALLEVNDLFEQTDLKTIKKIMHRAOTLLKCE 172
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Qy	173	CSVLLLED 180
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Qy 137 RALLEVVN 144
Db 131 SVALDVLS 138

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Search completed: June 13, 2003, 15:50:02
Job time : 6.52392 secs

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Best Local Similarity 29.7%; Pred. No. 6.1e-13;
Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;
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Qy 77 PTRSSDGETIGVAQAINKIPEGAPFETDEDEKVMQWYLPFCGTAISNAQLFAASRKEYERS 136
Db 72 PIWNSHQIIGVAQVNLRL-DGKPFDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKQ 130
Qy 137 RALLEVVN 144
Db 131 SVALDVLS 138

Query Match 19.1%; Score 186; DB 3; Length 490;
Best Local Similarity 29.7%; Pred. No. 9.3e-13;
Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;
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Db 12 SFKESMEKSSYSDWLNNSIAELVASTGLPVPVNISDAYQDPFDAEADQISGFHRSVLCV 71
Qy 77 PTRSSDGETIGVAQAINKIPEGAPFETDEDEKVMQWYLPFCGTAISNAQLFAASRKEYERS 136
Db 72 PIWNSHQIIGVAQVNLRL-DGKPFDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKQ 130
Qy 137 RALLEVVN 144
Db 131 SVALDVLS 138

RESULT 15
US-09-226-741-1
; Sequence 1, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-1 CIP
; CURRENT APPLICATION NUMBER: US/09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/226,741
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 367
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDE10A2
US-09-595-514-3

Query Match 19.1%; Score 186; DB 3; Length 490;
Best Local Similarity 29.7%; Pred. No. 9.3e-13;
Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;
Qy 34 SLAEKOEK--HQDFLIQROTQT-----KDRRFNDEIDKLTGYKTKSLLCM 76
Db 12 SFKESMEKSSYSDWLNNSIAELVASTGLPVPVNISDAYQDPFDAEADQISGFHRSVLCV 71
Qy 77 PTRSSDGETIGVAQAINKIPEGAPFETDEDEKVMQWYLPFCGTAISNAQLFAASRKEYERS 136
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Db 131 SVALDVLS 138

RESULT 15
US-09-226-741-1
; Sequence 1, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 490
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDE10A1
US-09-226-741-1

Query Match 19.1%; Score 186; DB 3; Length 490;
Best Local Similarity 29.7%; Pred. No. 9.3e-13;
Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;
Qy 34 SLAEKOEK--HQDFLIQROTQT-----KDRRFNDEIDKLTGYKTKSLLCM 76
Db 12 SFKESMEKSSYSDWLNNSIAELVASTGLPVPVNISDAYQDPFDAEADQISGFHRSVLCV 71
Qy 77 PTRSSDGETIGVAQAINKIPEGAPFETDEDEKVMQWYLPFCGTAISNAQLFAASRKEYERS 136
Db 72 PIWNSHQIIGVAQVNLRL-DGKPFDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKQ 130
Qy 137 RALLEVVN 144
Db 131 SVALDVLS 138

F:855/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 20.0%; Score 195; DB 2; Length 858;
Best Local Similarity 37.3%; Pred. No. 4.8e-08;
Matches 47; Conservative 23; Mismatches 54; Indels 2; Gaps 2;

QY 54 KDRRNDIDKLTGYTKSLKMPIRSSDGEIGVAQAINKIPEGAPTEDEKVMQYL 113
DB 160 KNSHFSDFMDKQGTGYTKNLATPTVVGK-EVLAVIMAVNKV-NASEFSKQDEEVFSYL 217
QY 114 PFCGTAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKRCRC 173
DB 218 NFVSIILRLHTSYWNIERSRQLLMSANKVFEELTDVERQHFHKAITYTTRVTLNCERY 277
QY 174 SVLLLE 179
DB 278 SIGLLD 283

RESULT 6

S06418
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine
N:Alternate names: cGMP phosphodiesterase alpha chain
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: S06418; S27007; S00161; A34611; S08516
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.; Zakharenko, I.V.; Lipkin, V.M.
Dokl. Biochem. 296, 303-307, 1987

A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpha chain
A:Reference number: S06418
A:Accession: S06418

A:Molecule type: mRNA
A:Residues: 1-859 <OV1>
A:Cross-references: EMBL:X12756; NID:g616; PIDN:CAA31243.1; PID:g617
A:Accession: S27007

A:Molecule type: protein
A:Residues: 2-11;22-27;32-40;95-98;112-115;180-193;248-267;275-282;297-306;312-330;361-364;564-661;663-667;703-712;734-736;751-760;766-771;787-798;811-819 <OV2>
A:Note: This paper is a translation of the Russian paper published in Dokl. Akad. Nauk SSSR, 1987.
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ischenko, K.A.; Zagranichny, V.E.; FEBS Lett. 223, 169-173, 1987

A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpha chain
A:Reference number: S00161; MUID:88030033; PMID:2822478
A:Accession: S00161

A:Molecule type: mRNA
A:Residues: 1-859 <OV2>
A:Cross-references: EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PID:g162828
A:Note: part of this sequence was confirmed by protein sequencing
A:Note: 381-val was also found
R:Pittler, S.J.; Baehr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuine, Genomics 6, 272-283, 1990

A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodiesterase
A:Reference number: A34611; MUID:90169986; PMID:2155175
A:Accession: A34611

A:Molecule type: mRNA
A:Residues: 1-193,'V',195-423,'T',425-674,'F',676-859 <PIT>
A:Cross-references: GB:M26043; NID:g162833; PIDN:AAA30443.1; PID:g162834
C:Comment: This protein is involved in the transduction and amplification of the visual signal.
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide phosphodiesterase
C:Keywords: acetylated amino end; cGMP; heterotrimer; phosphoric diester hydrolase; retina
F:2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <MA>
F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental

Query Match 19.8%; Score 193; DB 1; Length 859;
Best Local Similarity 34.1%; Pred. No. 7e-08;
Matches 43; Conservative 29; Mismatches 52; Indels 2; Gaps 2;

QY 54 KDRRNDIDKLTGYTKSLKMPIRSSDGEIGVAQAINKIPEGAPTEDEKVMQYL 113
DB 158 EDEHCFDVEDILTEYTKNLLASPIMNGK-DVVAIMAVNKV-DGPHEFTEENDEETLLKYL 215

QY 114 PFCGTAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKRCRC 173
DB 216 NFANLIMKVFHLSVLHNCETRRGQILLWSGSKVFEELTDIERQHFHKAITYTTRVRAFLNCDRY 275
QY 174 SVLLLE 179
DB 276 SVGLLD 281

RESULT 7

B34611
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 21-Jan-2000
C:Accession: B34611
R:Pittler, S.J.; Baehr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuine, Genomics 6, 272-283, 1990
A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodiesterase
A:Reference number: A34611; MUID:90169986; PMID:2155175
A:Accession: B34611

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-859 <PIT>

A:Cross-references: GB:M26061

C:Genetics:

A:Gene: GDB:PD66A; PDEA

A:Cross-references: GDB:120265; OMIM:180071

A:Map position: 5q31.2-5q34

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide phosphodiesterase
C:Keywords: cGMP binding; phosphoric diester hydrolase

F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 19.4%; Score 189; DB 2; Length 859;
Best Local Similarity 34.1%; Pred. No. 1.5e-07;
Matches 43; Conservative 29; Mismatches 52; Indels 2; Gaps 2;

QY 54 KDRRNDIDKLTGYTKSLKMPIRSSDGEIGVAQAINKIPEGAPTEDEKVMQYL 113
DB 158 EDEHCFDVEDILTEYTKNLLASPIMNGK-DVVAIMAVNKV-DGSHTFKRDEETLLKYL 215

QY 114 PFCGTAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKRCRC 173
DB 216 NFANLIMKVFHLSVLHNCETRRGQILLWSGSKVFEELTDIERQHFHKAITYTTRVRAFLNCDRY 275

QY 174 SVLLLE 179
DB 276 SVGLLD 281

RESULT 8

A47451
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C:Accession: A47451; S34290
R:Suber, M.L.; Pittler, S.J.; Qin, N.; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, Proc. Natl. Acad. Sci. U.S.A. 90, 3968-3972, 1993
A:Title: Irish setter dogs affected with rod/cone dysplasia contain a nonsense mutation
A:Reference number: A47451; MUID:93248211; PMID:8387203
A:Accession: A47451

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-856 <SUB>

A:Cross-references: GB:223014; NID:g312327

A:Experimental source: Irish setter, retina

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:130782, NCBI:130783)

R:Clements, P.J.

submitted to the EMBL Data Library, June 1993

A:Reference number: S34290

A:Accession: S34290

A:Status: preliminary

A:Molecule type: mRNA

C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AC2089
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2089
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-859 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073965.1; PID:gl7131357; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: cyb1

Query Match 17.9%; Score 174.5; DB 2; Length 859;
Best Local Similarity 35.9%; Pred. No. 2.2e-06;
Matches 42; Conservative 24; Mismatches 48; Indels 3; Gaps 2;
QY 54 KDRRENDEIDKLTGYKTKSLICMPITRSSDGEIIGVQAQINKIPEGAPTEDEDEKVMQMYL 113
DB 311 KDRPFDTTDRKTGYLTNRILCLPVFNSANELIGVTQLINK--QQGSFTASDEEFMRAFN 368
QY 114 PFCGIAISNAOLFASRKREYENSRALLEVVNDLPEEOTDLEKIVKIMHRAOTLLKC 170
DB 369 IQAGVALENARLFENVILEKQYQKDILQSLSDAV-ISTDMAGRIVTINDAALELLGC 424

Search completed: June 13, 2003, 15:49:43
Job time : 8.51253 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:38:49 ; Search time 3.97722 Seconds
(without alignments)
2023.123 Million cell updates/sec

Title: US-09-663-542-1_COPY_1_194

Perfect score: 975

Sequence: 1 MLKQARRPLFRNLSATQWK.....VLLLEDIESPVVVKTKSFEL 194

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	308.5	31.6	833	1	CNSA.RAT
2	307.5	31.5	865	1	CNSA.BOVIN
3	307.5	31.5	865	1	CNSA.CANFA
4	307.5	31.5	865	1	CNSA.HUMAN
5	205.5	21.1	862	1	CNRC.CHICK
6	195	20.0	855	1	CNRC.BOVIN
7	191	19.6	858	1	CNRC.HUMAN
8	189	19.4	858	1	CNRA.BOVIN
9	189	19.4	859	1	CNRA.HUMAN
10	183	18.8	854	1	CNRB.HUMAN
11	183	18.8	856	1	CNRB.CANFA
12	183	18.8	858	1	CNRA.MOUSE
13	183	18.8	860	1	CNRA.CANFA
14	180.5	18.5	393	1	YB2J.CAEEL
15	175	17.9	856	1	CNRB.MOUSE
16	170	17.4	853	1	CNRB.BOVIN
17	165	16.9	779	1	CN10.HUMAN
18	162	16.6	941	1	CN2A.HUMAN
19	159	16.3	928	1	CN2A.BOVIN
20	154	15.8	921	1	CN2A.CANFA
21	100	10.3	918	1	YNE6.CAEEL
22	86.5	8.9	1855	1	MY5A.HUMAN
23	86	8.8	496	1	IMDH.METJA
24	85.5	8.8	821	1	LIN5.CAEEL
25	84.5	8.7	1828	1	MY5A.RAT
26	84	8.6	2869	1	RBP1.PLAVB
27	82.5	8.5	1853	1	MY5A.MOUSE
28	82	8.4	859	1	MUTS.AQUAE
29	81.5	8.4	3726	1	TRX.DROME
30	81	8.3	2153	1	POLG.HRV16
31	80.5	8.3	3421	1	TEGU.HSVER
32	79.5	8.2	171	1	YF87.METJA
33	79	8.1	220	1	Y231.RICPR

RESULT 1

ID	CNSA.RAT	STANDARD;	PRT;	833 AA.
AC	O54735;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)			
DE	(CGMP-binding CGMP-specific phosphodiesterase).			
GN	PDE5A OR PDE5.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Lung;			
RX	MEDLINE=98036118; PubMed=9370351;			
RA	Kotera J., Yanaka N., Fujishige K., Imai Y., Akatsuka H., Ishizuka T.,			
RA	Kawashima K., Omori K.;			
RT	"Expression of rat CGMP-binding CGMP-specific phosphodiesterase mRNA			
RT	in Purkinje cell layers during postnatal neuronal development.";			
RL	Eur. J. Biochem. 249:434-442(1997).			
CC	FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE			
CC	INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS			
CC	PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-			
CC	GMP.			
CC	FUNCTION: CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =			
CC	guanosine 5'-phosphate.			
CC	COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR			
CC	CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).			
CC	PATHWAY: Cyclic nucleotide metabolism.			
CC	ALTERNATIVE PRODUCTS: 2 ISOFORMS; PDE5A1 AND PDE5A2 (SHOWN HERE);			
CC	ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO			
CC	POTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN			
CC	WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A			
CC	AND B.			
CC	PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO			
CC	ALLOSTERIC SITES (BY SIMILARITY).			
CC	SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE			
CC	FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL: D89093; BAA23672.1;			
DR	InterPro: IPR003018; GAF.			
DR	InterPro: IPR003607; ME_Pplase_HDC.			
DR	InterPro: IPR002073; PDEase.			

DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDG; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CGMP; CGMP-binding; Phosphorylation; Alternative splicing;
Zinc; Repeat.
FT NP_BIND 196 279 CGMP (BY SIMILARITY).
FT NP_BIND 378 468 CGMP (BY SIMILARITY).
FT BINDING 244 244 CGMP (BY SIMILARITY).
FT BINDING 245 245 CGMP (BY SIMILARITY).
FT BINDING 257 257 CGMP (BY SIMILARITY).
FT BINDING 446 446 CGMP (BY SIMILARITY).
FT DOMAIN 546 811 CATALYTIC (BY SIMILARITY).
FT MOD_RES 60 60 PHOSPHORYLATION (POTENTIAL).
FT METAL 571 571 ZINC 1 (POTENTIAL).
FT METAL 575 575 ZINC 1 (POTENTIAL).
FT METAL 600 600 ZINC 1 (POTENTIAL).
FT METAL 611 611 ZINC 2 (POTENTIAL).
FT METAL 615 615 ZINC 2 (POTENTIAL).
FT METAL 640 640 ZINC 2 (POTENTIAL).
SQ SEQUENCE 833 AA; 94556 MW; 712DC159C80CB09D CRC64;
Query Match 31.6%; Score 308.5; DB 1; Length 833;
Best Local Similarity 43.7%; Pred. No. 1.7e-18;
Matches 62; Conservative 34; Mismatches 43; Indels 3; Gaps 2;
QY 54 KDRRENDEIDKLTGYKTKSLCLMPTRSSDGEIIGVQAQAIN-KIPGAPFTEDDEKVMQMY 112
DB 205 EDPRNEAEVDQITGYKTSILCMPIKNHREEVGVQAQINKSGNGGFTTEKDEKFAAY 264
QY 113 LPFCGIATISNAQLFAASKEYERSRALLVNDLPFEOTDLEKIVKTHMRAQTLLKCEK 172
DB 265 LAFCGIVLHNAQLYTSILEKRNQVLLDLASLIFEQOQSLEVLTKTAANTIIISMVQVK 324
QY 173 CSQLLEDIESPVVKFTKSFEL 194
DB 325 CTIFIVD--EDCPDSFSRVQM 344

RESULT 2

CNSA_BOVIN
ID CNSA_BOVIN STANDARD; PRT; 865 AA.
AC Q28156;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
DE (CGMP-binding CGMP-specific phosphodiesterase).
GN PDE5A OR PDE5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=94043054; PubMed=8226796;
RA McAllister-Lucas L.M., Sonnenburg W.K., Kadlecsek A., Seger D.,
RA Trong H.L., Colbran J.L., Thomas M.K., Walsh K.A., Francis S.H.,
RA Corbin J.D., Beavo J.A.;
RT "The structure of a bovine lung CGMP-binding, CGMP-specific
phosphodiesterase deduced from a cDNA clone.";
RL J. Biol. Chem. 268:22863-22873(1993).
RN [2]
RP METAL-BINDING.
RX MEDLINE=94357882; PubMed=8077192;
RA Francis S.H., Colbran J.L., McAllister-Lucas L.M., Corbin J.D.;
RT "Zinc interactions and conserved motifs of the CGMP-binding CGMP-
specific phosphodiesterase suggest that it is a zinc hydrolase.";
RL J. Biol. Chem. 269:22477-22480(1994).
RN [3]
RP MUTAGENESIS.
RX MEDLINE=96107229; PubMed=8530505;
RA McAllister-Lucas L.M., Haik T.L., Colbran J.L., Sonnenburg W.K.,
RA Seger D., Turko I.V., Beavo J.A., Francis S.H., Corbin J.D.;
RT "An essential aspartic acid at each of two allosteric CGMP-binding
sites of a CGMP-specific phosphodiesterase.";
RL J. Biol. Chem. 270:30671-30679(1995).
RN [4]
RP MUTAGENESIS.
RX MEDLINE=96355629; PubMed=8703039;
RA Turko I.V., Haik T.L., McAllister-Lucas L.M., Burns F., Francis S.H.,
RA Francis S.H., Corbin J.D.;
RT "Identification of key amino acids in a conserved CGMP-binding site of
CGMP-binding phosphodiesterases. A putative NKxnd motif for CGMP
binding.";
RL J. Biol. Chem. 271:22240-22244(1996).
RN [5]
RP PHOSPHORYLATION, AND MUTAGENESIS.
RX MEDLINE=98109724; PubMed=9445376;
RA Turko I.V., Francis S.H., Corbin J.D.;
RT "Binding of CGMP to both allosteric sites of CGMP-binding CGMP-
specific phosphodiesterase (PDE5) is required for its
phosphorylation.";
RL Biochem. J. 329:505-510(1998).
CC -!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-
GMP.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
guanosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT
CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS.
CC -!- ENZYME REGULATION: MOST POTENTLY INHIBITED BY ZAPRINAST AND
DIPYRIDAMOLE.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
AND B.
CC -!- PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
ALLOSTERIC SITES.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
EMBL; L16545; AAB00990.1;
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDG; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CGMP; CGMP-binding; Phosphorylation; Zinc; Repeat.
FT MOD_RES 92 92 PHOSPHORYLATION (POTENTIAL).
FT METAL 603 603 ZINC 1 (POTENTIAL).
FT METAL 607 607 ZINC 1 (POTENTIAL).
FT METAL 632 632 ZINC 1 (POTENTIAL).
FT METAL 643 643 ZINC 2 (POTENTIAL).
FT METAL 647 647 ZINC 2 (POTENTIAL).
FT METAL 672 672 ZINC 2 (POTENTIAL).
FT NP_BIND 228 311 CGMP.

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FT NP_BIND 410 500 CGMP.
FT BINDING 276 276 CGMP.
FT BINDING 277 277 CGMP.
FT BINDING 289 289 CGMP.
FT BINDING 478 478 CGMP.
FT DOMAIN 578 843 CATALYTIC (BY SIMILARITY).
FT MUTAGEN 276 276 N->A: DECREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY.
FT MUTAGEN 277 277 K->A: DECREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY.
FT MUTAGEN 277 277 K->R: SLIGHT INCREASE IN CGMP-BINDING.
FT MUTAGEN 289 289 D->A: DECREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY.
FT MUTAGEN 289 289 D->N: INCREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY.
FT MUTAGEN 290 290 E->A: NO CHANGE IN CGMP-BINDING.
FT MUTAGEN 478 478 D->A: INCREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY. PHOSPHORYLATED AT
LOWER CONCENTRATIONS OF CGMP.
SQ SEQUENCE 865 AA; 98626 MW; 2FF7144B2990B4F7 CRC64;

Query Match 31.5%; Score 307.5; DB 1; Length 865;
Best Local Similarity 46.1%; Pred. No. 2.2e-18;
Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;

QY 54 KDRFNDEIDKLTGYKTSLLCMPISRSDGEIIGVAQAIN-KIPEGAPFTDEDEKVMQMY 112
DB 237 EDPRNAEVDQITGYKTQSILCMPIKNHREEVGVGAQAINKSGNGGFTTEKDEKDFAA 296

QY 113 LPFGGIALSNAQLFAASRKEYERSALLLEVNDLFEEQTDLEKIVKIMHRAOTLLKCE 172
DB 297 LAFCCIVLHNAQLYETSLLENKRQVLLDLASLIFEEOQSLEVLKIAATIIISFMQVOK 356

QY 173 CSVLLED 180
DB 357 CTIFIVDE 364

RESULT 3
ID CNSA_CANFA STANDARD; PRT; 865 AA.
AC 077746; 077747;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
DE (CGMP-binding CGMP-specific phosphodiesterase).
GN PDE5A OR PDE5.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS PDE5A1 AND PDE5A2).
RC TISSUE=Lung;
RX MEDLINE=98434620; PubMed=9756948;
RA Kotera J., Fujishige K., Akatsuka H., Inai Y., Yanaka N., Omori K.;
RT "Novel alternative splice variants of CGMP-binding CGMP-specific
RT phosphodiesterase."
RL J. Biol. Chem. 273:26982-26990(1998).
CC -!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
CC INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
CC PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-
CC GMP.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2O) =
CC guanosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
CC MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT
CC CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).
CC -!- ENZYME REGULATION: INHIBITED BY ZAPRINAST.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- SUBCELLULAR LOCATION: PDE5A1 AND PDE5A2 ARE LOCATED MOSTLY TO
CC SOLUBLE CELLULAR FRACTIONS AND SOME TO PARTICULATE CELLULAR

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CC FRACTIONS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PDE5A1 (SHOWN HERE) AND PDE5A2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: BOTH ISOFORMS EXPRESSED ABUNDANTLY IN THE
CC CEREBELLUM, HIPPOCAMPUS, RETINA, LUNG, HEART, SPLEEN AND THORACIC
CC ARTERY. PDE5A1, BUT NOT PDE5A2, IS ALSO ABUNDANTLY EXPRESSED IN
CC THE PYLORUS.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
CC WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
CC AND B.
CC -!- PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
CC ALLOSTERIC SITES (BY SIMILARITY).
CC -!- MISCELLANEOUS: CGMP-BINDING TO THE ALLOSTERIC SITES IS STIMULATED
CC BY 3-ISOBUTYL-1-METHYLXANTHINE (IBMX).
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB008467; BAA33503.1; -
CC EMBL; AB008468; BAA33504.1; -
CC InterPro; IPR003018; GAF;
CC InterPro; IPR003607; ME_Plpase_HDC.
CC InterPro; IPR002073; PDEase.
CC Pfam; PF00233; PDEase; 1.
CC Pfam; PF01590; GAF; 2.
CC PRINTS; PR00387; PD1ESTERASE1.
CC SMART; SM00065; GAF; 2.
CC SMART; SM00471; HDC; 1.
CC PROSITE; PS00126; PDEASE_I; 1.
CC Hydrolase; CGMP; CGMP-binding; Phosphorylation; Alternative splicing;
KW Zinc; Repeat.
FT NP_BIND 228 311 CGMP (BY SIMILARITY).
FT NP_BIND 410 500 CGMP (BY SIMILARITY).
FT BINDING 276 276 CGMP (BY SIMILARITY).
FT BINDING 277 277 CGMP (BY SIMILARITY).
FT BINDING 289 289 CGMP (BY SIMILARITY).
FT BINDING 478 843 CGMP (BY SIMILARITY).
FT DOMAIN 578 843 CATALYTIC (BY SIMILARITY).
FT MOD_RES 92 92 PHOSPHORYLATION (POTENTIAL).
FT METAL 603 603 ZINC 1 (POTENTIAL).
FT METAL 607 607 ZINC 1 (POTENTIAL).
FT METAL 632 632 ZINC 1 (POTENTIAL).
FT METAL 643 643 ZINC 2 (POTENTIAL).
FT METAL 647 647 ZINC 2 (POTENTIAL).
FT METAL 672 672 ZINC 2 (POTENTIAL).
FT VARSPLIC 1 40 MERGSPGAGAAALPRDQDSVEALDDHDDHDDFTSFYVKKAT
FT -> MLFPGHQR (IN ISOFORM PDE5A2).
SQ SEQUENCE 865 AA; 98293 MW; F20BB37B71E93BB6 CRC64;

Query Match 31.5%; Score 307.5; DB 1; Length 865;
Best Local Similarity 46.1%; Pred. No. 2.2e-18;
Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;

QY 54 KDRFNDEIDKLTGYKTSLLCMPISRSDGEIIGVAQAIN-KIPEGAPFTDEDEKVMQMY 112
DB 237 EDPRNAEVDQITGYKTQSILCMPIKNHREEVGVGAQAINKSGNGGFTTEKDEKDFAA 296

QY 113 LPFGGIALSNAQLFAASRKEYERSALLLEVNDLFEEQTDLEKIVKIMHRAOTLLKCE 172
DB 297 LAFCCIVLHNAQLYETSLLENKRQVLLDLASLIFEEOQSLEVLKIAATIIISFMQVOK 356

QY 173 CSVLLED 180
DB 357 CTIFIVDE 364

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QY 54 KDRRENDEIKLTYKTKSLCMLPIRSDDGEIIGVAQAIN-KIPGAPFTEDEKVMQY 112
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 EDPREAEVDQITGYKTKSLCMLPIKHNREUVGVQAINKSNGGTFTEKDEKFRAY 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 113 LPFGCIATSNALQFAASKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCE 172
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 LAFCVILHNAQLYETSLENKRNOVLDSLAFIEEQSLEVLKIAATIISPMQVOK 366
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 173 CSVLLED 180
:|||||:
Db 367 CTIFIVDE 374

RESULT 5
CNRC_CHICK STANDARD; PRT; 862 AA.
ID CNRC_CHICK
AC P52731;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
DE (EC 3.1.4.17).
OS PDE6C.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rhode Island red; TISSUE=Retina;
RX MEDLINE=95121406; PubMed=7821382;
RA Sample=Rowland S.L., Green D.A.;
RT "Molecular characterization of the alpha'-subunit of cone
RT photoreceptor cGMP phosphodiesterase in normal and rd chicken.";
RL Exp. Eye Res. 59:365-372(1994).
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED
CC WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 KDa.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L29233; AAC4223.1; -
CC InterPro; IPR003018; GAF.
CC InterPro; IPR003607; ME.Pplase_Hdc.
CC InterPro; IPR002073; PDEase.
CC InterPro; IPR001230; Prenyl_site.
CC Pfam; PF00233; PDEase; 1.
CC Pfam; PF01590; GAF; 2.
CC PRINTS; SM00065; GAF; 2.
CC SMART; SM00471; Hdc; 1.
CC PROSITE; PS00126; PDASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
FT LIPID 859 859 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 862 AA; 100008 MW; B03145B5FF826A8 CRC64;

Query Match 21.1%; Score 205.5; Db 1; Length 862;
Best Local Similarity 29.4%; Pred. No. 8.5e-10;
Matches 53; Conservative 34; Mismatches 60; Indels 33; Gaps 4;
QY 25 TRLVQISGASLAEKQKHODFLIQROTQT-----KDRRFN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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```
Db 112 TRLVNVTPTS-----KFEDNLVNPDKETVPFLDIGIAGVVAHTKKFFNIPDVKKNNHFS 165
QY 60 DEIDKLTGYKTKSLCMLPIRSDDGEIIGVAQAINKIPGAPFTEDEKVMQYLPFCGIA 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166 DYLDKKTGTVTNNMAIPI-TQGEVLAVVWALNKL-NASEFSKDEDEVEFKYLFISLV 223
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 ISNAOLFASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCEKRCVLLLE 179
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 224 LRNHHTSVLYNIESRRSQMLLSANKVFEELTDIERQFHKALYTTIRMYLNCERYSVGLLD 283

RESULT 6
CNRC_BOVIN STANDARD; PRT; 855 AA.
ID CNRC_BOVIN
AC P16586;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
DE (EC 3.1.4.17) (PDE V-C1).
GN PDE6C OR PDEA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90115860; PubMed=2153291;
RA Li T., Volpp K., Applebury M.L.;
RT "Bovine cone photoreceptor cGMP phosphodiesterase structure deduced
RT from a cDNA clone.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:293-297(1990).
RN [2]
RP SEQUENCE OF 308-502 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=90115859; PubMed=2153290;
RA Charbonneau H., Prusti R.K., Letrong H., Sonnenburg W.K.,
RA Mullaney P.J., Walsh K., Beavo J.A.;
RT "Identification of a noncatalytic cGMP-binding domain conserved in
RT both the cGMP-stimulated and photoreceptor cyclic nucleotide
RT phosphodiesterases.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:288-292(1990).
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED
CC WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 KDa.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC
CC EMBL; M37838; AAA30687.1; -
CC EMBL; M33140; AAA30688.1; -
CC PIR; A34810; A34810.
CC InterPro; IPR003018; GAF.
CC InterPro; IPR003607; ME.Pplase_Hdc.
CC InterPro; IPR002073; PDEase.
CC InterPro; IPR001230; Prenyl_site.
CC Pfam; PF00233; PDEase; 1.
CC Pfam; PF01590; GAF; 2.
CC PRINTS; SM00387; PDIESTERASE1.
CC SMART; SM00065; GAF; 2.
CC SMART; SM00471; Hdc; 1.
CC PROSITE; PS00126; PDASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
FT LIPID 852 852 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 855 AA; 98797 MW; 1FCFFD045686D65 CRC64;
```

Query Match 20.0%; Score 195; DB 1; Length 855;
 Best Local Similarity 36.5%; Pred. No. 6.5e-09;
 Matches 46; Conservative 25; Mismatches 53; Indels 2; Gaps 2;

QY 54 KDRFNDEIDKLTGYKTSKLLCMPIRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQMYL 113
 DB 155 KNSHSDFMKDTGYVTNLLATPIVMGK-EVLAVFMAVNV-NASEFSKQDEEVFSKYL 212

QY 114 PFCGTAISNAQLFAASRKEYERSALLVNDLFEEDTDLKIVKIMHRAQTLLKCERC 173
 DB 213 SEVSIILKHTNYLYNIESRRSQILMWSANKVFEELTDVERQPHKALYTVRTYLNCERY 272

QY 174 SVLLLE 179
 DB 273 SIGLLD 278

RESULT 7

CNRC_HUMAN STANDARD; PRT; 858 AA.
 AC P51160;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
 DE (EC 3.1.4.17).
 GN PDE6C OR PDEA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=96039253; PubMed=7490077;
 RC TISSUE=Retina;
 RA Piriev N.I., Viczian A.S., Ye J., Kerner B., Korenberg J.R.,
 RA Farber D.B.;
 RT "Gene structure and amino acid sequence of the human cone
 RT photoreceptor cGMP-phosphodiesterase alpha' subunit (PDEA2) and its
 RT chromosomal localization to 10q24.";
 RL Genomics 28:429-435(1995).
 RN [2]

SEQUENCE FROM N.A.

RA Piriev N.I., Viczian A., Ye J., Farber D.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]

SEQUENCE FROM N.A.

RC TISSUE=Retina;
 RA Feshchenko E.A.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC 1- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O -
 CC guanosine 5'-phosphate.
 CC 2- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED
 CC WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 KDa.
 CC 3- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.

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DB EMBL; U31973; AAA96392.1; -
 DR EMBL; U20212; AAA92886.1; -
 DR EMBL; U20196; AAA92886.1; JOINED.
 DR EMBL; U20197; AAA92886.1; JOINED.
 DR EMBL; U20199; AAA92886.1; JOINED.
 DR EMBL; U20200; AAA92886.1; JOINED.
 DR EMBL; U20201; AAA92886.1; JOINED.

DR EMBL; U20202; AAA92886.1; JOINED.
 DR EMBL; U20203; AAA92886.1; JOINED.
 DR EMBL; U20204; AAA92886.1; JOINED.
 DR EMBL; U20205; AAA92886.1; JOINED.
 DR EMBL; U20206; AAA92886.1; JOINED.
 DR EMBL; U20207; AAA92886.1; JOINED.
 DR EMBL; U20208; AAA92886.1; JOINED.
 DR EMBL; U20209; AAA92886.1; JOINED.
 DR EMBL; U20210; AAA92886.1; JOINED.
 DR EMBL; U20211; AAA92886.1; JOINED.
 DR EMBL; X94354; CAA64079.1; -
 DR MIM; 600827; -
 DR InterPro; HGNC:8787; PDE6C.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR003607; ME_Pplase_HDC.
 DR InterPro; IPR002073; PDEase.
 DR InterPro; IPR001230; Prenyl_site.
 DR Pfam; PF00233; PDEase; 1.
 DR Pfam; PF01590; GAF; 2.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR SMART; SM00065; GAF; 2.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
 FT LIPID 855 855
 FT CONFLICT 116 116 V -> D (IN REF. 3).
 FT CONFLICT 270 270 S -> T (IN REF. 3).
 FT CONFLICT 373 373 Q -> P (IN REF. 1).
 FT CONFLICT 464 464 P -> L (IN REF. 1).
 FT CONFLICT 565 565 Q -> R (IN REF. 3).
 SQ SEQUENCE 858 AA; 99102 MW; 3D1535C21780A56E CRC64;

Query Match 19.6%; Score 191; DB 1; Length 858;

Best Local Similarity 36.5%; Pred. No. 1.4e-08;

Matches 46; Conservative 24; Mismatches 54; Indels 2; Gaps 2;

QY 54 KDRFNDEIDKLTGYKTSKLLCMPIRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQMYL 113
 DB 150 KNSHSDFMKDTGYVTNLLATPIVMGK-EVLAVFMAVNV-NASEFSKQDEEVFSKYL 217

QY 114 PFCGTAISNAQLFAASRKEYERSALLVNDLFEEDTDLKIVKIMHRAQTLLKCERC 173
 DB 218 NEVSIILKHTNYLYNIESRRSQILMWSANKVFEELTDVERQPHKALYTVRSYLNCERY 277

QY 174 SVLLLE 179
 DB 278 SIGLLD 283

RESULT 8

CNRA_BOVIN STANDARD; PRT; 858 AA.
 AC P11541;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
 DE (EC 3.1.4.17) (GMP-PDE alpha) (PDE V-B1).
 GN PDE6A OR PDEA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=90169986; PubMed=2155175;
 RA Pittler S.J., Baehr W., Wasmuth J.J., McConnell D.G., Champagne M.S.,
 RA Vautuinen P., Ledbetter D., Davis R.L.;
 RT "Molecular characterization of human and bovine rod photoreceptor
 RT cGMP phosphodiesterase alpha-subunit and chromosomal localization of
 RT the human gene.";
 RL Genomics 6:272-283(1990).


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DR PIR; B34611; B34611.
DR Genew; HGNC:8785; PDE6A.
DR MIM; 180071; .
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Plipase_HDC.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein;
KW Retinitis pigmentosa; Disease mutation.
FT INIT MET 0
FT LIPID 856 856 FARNESYL (BY SIMILARITY).
FT VARIANT 343 343 S -> R (IN ARRP).
FT /FTID=VAR_006049.
SQ SEQUENCE 859 AA; 99503 MW; 983C361334D58414 CRC64;

Query Match 19.4%; Score 189; DB 1; Length 859;
Best Local Similarity 34.1%; Pred. No. 2.1e-08;
Matches 43; Conservative 29; Mismatches 52; Indels 2; Gaps 2;

QY 54 KDRFNDEIDKLTGYKTKSLCPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYL 113
DB 157 EDEHFCDFVDILTETKTKNILASPIMNGK-DVAILMAVNV-DGSHTKRDDEILLKYL 214

QY 114 PFCGTAINAQLFRASRKEYERSRALLVVDLFEQTDLEKIYKIMHRAQTLLKCRC 173
DB 215 NFANLIMKYHLSYLHNCETRGQILLWSGKVFELTDIERQPHKALYTVRAFLNCRDY 274

QY 174 SVLLLE 179
DB 275 SVGLLD 280

RESULT 10
CNRB HUMAN
ID CNRB HUMAN STANDARD; PRT; 854 AA.
AC P35913; Q9BWH5;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rod cGMP-specific 3',5'-cyclic phosphodiesterase beta-subunit
DE (EC 3.1.4.17) (GMP-PDE beta).
GN PDE6B OR PDEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93351644; PubMed=8394243;
RA Khrantsov N.V., Feshchenko E.A., Suslova V.A., Shmukler B.E.,
RA Terpugov B.E., Rakitina T.V., Atabekova N.V., Lipkin V.M.;
RT "The human rod photoreceptor cGMP phosphodiesterase beta-subunit.
RT Structural studies of its cDNA and gene.";
RL FEBS Lett. 327:275-278(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93244036; PubMed=1338685;
RA Khrantsov N.V., Feshchenko E.A., Suslova V.A., Terpugov B.E.,
RA Rakitina T.V., Atabekova N.V., Shmukler B.E., Lipkin V.M.;
RT "Structural studies of cDNA and the gene for the beta-subunit of cGMP
RT phosphodiesterase from human retina.";
RL Bioorg. Khim. 18:1551-1554(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;

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RX MEDLINE=92347868; PubMed=1322354;
RA Collins C., Hutchinson G., Kowbel D., Riess O., Weber B., Hayden M.R.;
RT "The human beta-subunit of rod photoreceptor cGMP phosphodiesterase:
RT complete retinal cDNA sequence and evidence for expression in brain.";
RL Genomics 13:698-704(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92066478; PubMed=1720239;
RA Weber B., Riess O., Hutchinson G., Collins C., Lin B., Kowbel D.,
RA Andrew S., Schappert K., Hayden M.R.;
RT "Genomic organization and complete sequence of the human gene encoding
RT the beta-subunit of the cGMP phosphodiesterase and its localisation to
RT 4p16.3.";
RL Nucleic Acids Res. 19:6263-6268(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 238-854 FROM N.A.
RC TISSUE=Retinal rod cell;
RX MEDLINE=96330350; PubMed=8768262;
RA Suslova V.A., Suslov O.N., Kim E.E., Lipkin V.M.;
RT "Organization of the gene for the beta-subunit of human photoreceptor
RT cyclic GMP phosphodiesterase.";
RL Bioorg. Khim. 22:256-263(1996).
RN [7]
RP VARIANT ADPR TYR-557.
RX MEDLINE=93350628; PubMed=8394174;
RA McLaughlin M.E., Sandberg M.A., Berson E.L., Dryja T.P.;
RT "Recessive mutations in the gene encoding the beta-subunit of rod
RT phosphodiesterase in patients with retinitis pigmentosa.";
RL Nat. Genet. 4:130-134(1993).
RN [8]
RP VARIANT CSNB3 ASN-258.
RX MEDLINE=94355978; PubMed=8075643;
RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
RT "Heterozygous missense mutation in the rod cGMP phosphodiesterase
RT beta-subunit gene in autosomal dominant stationary night blindness.";
RL Nat. Genet. 7:64-68(1994).
RN [9]
RP ERRATUM.
RX MEDLINE=95038845; PubMed=7951329;
RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
RL Nat. Genet. 7:551-551(1994).
RN [10]
RP VARIANT ARRP ASP-576.
RX MEDLINE=96125294; PubMed=8595886;
RA Danciger M., Blaney J., Gao Y.Q., Zhao D.Y., Heckenlively J.R.,
RA Jacobson S.G., Farber D.B.;
RT "Mutations in the PDE6B gene in autosomal recessive retinitis
RT pigmentosa.";
RL Genomics 30:1-7(1995).
RN [11]
RP VARIANTS ADPR LYS-166; HIS-212 AND HIS-228.
RX MEDLINE=96273603; PubMed=8698075;
RA Gao Y.Q., Danciger M., Zhao D.Y., Blaney J., Pirliev N.I., Shih J.,
RA Jacobson S.G., Heckenlively J.H., Farber D.B.;
RT "Screening of the PDE6B gene in patients with autosomal dominant
RT retinitis pigmentosa.";
RL Exp. Eye Res. 62:149-154(1996).
RN [12]
RP VARIANT ARRP ARG-699.
RX MEDLINE=96140746; PubMed=8557257;
RA Valverde D., Solans T., Grinberg D., Balcells S., Vilageliu L.,
RA Bayes M., Chivelet P., Besmond C., Goossens M., Gonzalez-Duarte R.,
RA Balget M.;
RT "A novel mutation in exon 17 of the beta-subunit of rod
RT phosphodiesterase in two RP sisters of a consanguineous family.";
RL Hum. Genet. 97:35-38(1996).
RN [13]
RP VARIANT ARRP GLN-552.

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RX MEDLINE=97114306; PubMed=8956055;
RA Valverde D., Balget M., Seminago R., del Rio E., Garcia-Sandoval B.,
RA del Rio T., Bayes M., Balcells S., Martinez A., Grinberg D., Ayuso C.,
RT "Identification of a novel R552Q mutation in exon 13 of the
RT beta-subunit of rod phosphodiesterase gene in a Spanish family with
RT autosomal recessive retinitis pigmentosa.";
RL Hum. Mutat. 8:393-394(1996).
RN [14]
RP VARIANT ARRP ASN-535.
RX MEDLINE=98205225; PubMed=9543643;
RA Saga M., Mashima Y., Akeo K., Kudoh J., Oguchi Y., Shimizu N.;
RT "A novel homozygous Ile535Asn mutation in the rod cGMP
RT phosphodiesterase beta-subunit gene in two brothers of a Japanese
RT family with autosomal recessive retinitis pigmentosa.";
RL Curr. Eye Res. 17:332-335(1998).
CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
CC FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF RETINITIS PIGMENTOSA
CC OF RETINAL PHOTORECEPTOR CELLS. PATIENTS TYPICALLY HAVE NIGHT
CC VISION BLINDNESS AND LOSS OF MIDPERIPHERAL VISUAL FIELD; AS THEIR
CC CONDITION PROGRESSES, THEY LOOSE THEIR FAR PERIPHERAL VISUAL FIELD
CC AND EVENTUALLY CENTRAL VISION AS WELL. RP MAY OCCUR WITH AUTOSOMAL
CC RECESSIVE (20-25% OF CASES; ARRP) AUTOSOMAL DOMINANT (15-20% OF
CC CASES; ADPR) OR X-LINKED (10-15% OF CASES; XRP) INHERITANCE.
CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF CONGENITAL STATIONARY
CC NIGHT BLINDNESS (CSNB3).
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -!- DATABASE: NAME-Mutations of the PDE6A/B/G genes;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.retina-international.com/sci-news/pdemut.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S41458; AB22690.1; -;
DR EMBL; X66142; CAA46932.1; -;
DR EMBL; X62692; CAA44569.1; -;
DR EMBL; X62693; CAA44569.1; JOINED.
DR EMBL; X62694; CAA44569.1; JOINED.
DR EMBL; X62695; CAA44569.1; JOINED.
DR EMBL; X90587; CAA62215.1; -;
DR EMBL; X90588; CAA62215.1; JOINED.
DR EMBL; X90589; CAA62215.1; JOINED.
DR EMBL; X90590; CAA62215.1; JOINED.
DR EMBL; BC000249; AAH00249.1; -;
DR PIR; A42828; A42828.
DR PIR; S34590; S34590.
DR Genew; HGNC:8786; PDE6B.
DR MTM; 180072; -;
DR MTM; 268000; -;
DR MIM; 163500; -;
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDease.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00233; PDease; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.

DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CGMP; Vision; Prenylation; Lipoprotein; Membrane;
KW Retinitis pigmentosa; Disease mutation
FT CHAIN 1 851 ROD CGMP-SPECIFIC 3',5'-CYCLIC
FT PHOSPHODIESTERASE BETA-SUBUNIT.
FT REMOVED IN MATURE FORM (BY SIMILARITY).
FT GERANYL-GERANYL (BY SIMILARITY).
FT R -> C (IN ARRP).
FT /FTID=VAR_009283.
FT E -> K (IN ADPR).
FT /FTID=VAR_009284.
FT Y -> H (IN ADPR).
FT /FTID=VAR_009285.
FT Y -> H (IN ARRP).
FT /FTID=VAR_009286.
FT L -> H (IN ADPR AND ARRP).
FT /FTID=VAR_009287.
FT L -> I.
FT /FTID=VAR_009288.
FT H -> N (IN CSNB3).
FT /FTID=VAR_009289.
FT
Query Match. 18.8%; Score 183; DB 1; Length 854;
Best Local Similarity 36.9%; Pred. No. 6.6e-08;
Matches 45; Conservative 20; Mismatches 55; Indels 2; Gaps 2;
QY 58 FNDEIDKLTGVTKSLCLMPTIRSSDGIIGVAAQAINKIPECAPPTDEDEKVMQWYLPFCG 117
DB 160 FSSFADELTDYKYNMLATPIMNCK-DVAVAVIMAVNKL-NGPFTSEDEDFVLYLNAT 217
QY 118 IATISNAQLFAASKEYERSRALLLEVNDLEFQTDLEKIVKIMHRAQTLLKCRCSVLL 177
DB 218 LYLKIYHLSYLHNCETRRGQVLLMSANKVFEELTDIERQHFAPYTVRAYLNCERYSVGL 277
QY 178 LE 179
DB 278 LD 279
RESULT 11
CNRB_CANFA STANDARD; PRT; 856 AA.
ID CNRB_CANFA
AC P33726;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Rod CGMP-specific 3',5'-cyclic phosphodiesterase beta-subunit
DE (EC 3.1.4.17) (GMP-PDE beta).
GN PDE6B OR PDEB OR PDBS.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Flissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Red setter; TISSUE=Retina;
RX MEDLINE=93248211; PubMed=8387203;
RA Suber M.L., Pittler S.J., Qin N., Wright G.C., Holcombe V.,
RA Lee R.H., Craft C.M., Lolley R.N., Baehr W.B., Hurwitz R.L.;
RT "Irish setter dogs affected with rod/cone dysplasia contain a nonsense
RT mutation in the rod cGMP phosphodiesterase beta-subunit gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:3968-3972(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Boxer X Doberman; TISSUE=Retina;
RA Clements P.J.;
CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
CC FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND

```

CC      BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC      -!- SUBCELLULAR LOCATION: Membrane-associated.
CC      -!- DISEASE: IRISH SETTER DOGS AFFECTED WITH ROD/CONE DYSPLASIA (RCD1)
CC      CONTAIN A NOISE MUTATION IN THE GENE THAT GIVES RISE TO A
CC      PROTEIN OF 807 AA LACKING 49 AA IN THE C-TERMINAL.
CC      -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC      FAMILY.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; 223014; CA80557.1; -
CC      EMBL; L13262; AAA30882.1; ALT_SEQ.
CC      PIR; S34290; S34290.
CC      InterPro; IPR003018; GAF.
CC      InterPro; IPR003607; ME_Pplase_Hdc.
CC      InterPro; IPR002073; PDEase.
CC      InterPro; IPR001230; Prenyl_site.
CC      Pfam; PF00233; PDEase; 1.
CC      Pfam; PF01590; GAF; 2.
CC      PRINTS; PR00387; PDIESTERASE1.
CC      SMART; SM00065; GAF; 2.
CC      SMART; SM00471; HDC; 1.
CC      PROSITE; PS00126; PDEASE_I; 1.
CC      Hydrolase; CGMP; Vision; Prenylation; Lipoprotein; Membrane;
CC      CHAIN 1 853 ROD CGMP-SPECIFIC 3',5'-CYCLIC
CC      PROPEP 854 856 PHOSPHODIESTERASE BETA-SUBUNIT.
CC      LIPID 853 853 REMOVED IN MATURE FORM (BY SIMILARITY).
CC      SEQUENCE 856 AA; 98461 MW; AC9D03F64D18A132 CRC64;
CC
CC      Query Match 18.8%; Score 183; DB 1; Length 856;
CC      Best Local Similarity 33.6%; Pred. No. 6.7e-08;
CC      Matches 45; Conservative 27; Mismatches 60; Indels 2; Gaps 2;
CC
CC      QY 46 LIQRTKTKRRFNDEIDKLTGYTKSLLCMPIRSSDGEIIGVAQAANKIPGAPFTEDEKVMOMYL 105
CC      DB 148 MNVQDVTECPHFSPFADELGYETRNILATPIMNGK-DVVAVIMALKL-DGPCFTFSED 205
CC      QY 106 EKVQMVLPGFCIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQ 165
CC      DB 206 EDVLKYLNFGLTKIYHLSYLNHCETRRGQVLLWSANKVFEELTDIERQFHKAFTVR 265
CC      QY 166 TLLKRCRCVLLLE 179
CC      DB 266 AYLNCNDRYSVGLLD 279
CC
CC      RESULT 12
CC      CNRA_MOUSE
CC      ID CNRA_MOUSE STANDARD; PRT; 858 AA.
CC      AC P27664;
CC      DT 01-AUG-1992 (Rel. 23, Created)
CC      DT 01-AUG-1992 (Rel. 23, Last sequence update)
CC      DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC      DE Rod CGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
CC      DE (EC 3.1.4.17) (GMP-PDE alpha).
CC      GN PDE6A OR PDEA OR MPA.
CC      OS Mus musculus (Mouse).
CC      OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC      OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CC      OX NCBI_TaxID=10090;
CC      [1]
CC      RN SEQUENCE FROM N.A.
CC      RP TISSUE=Retina;
CC      RX MEDLINE=91130581; Pubmed=1847109;
CC      RA Baehr W., Champagne M.S., Lee A.K., Pittler S.J.;

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RT      "Complete cDNA sequences of mouse rod photoreceptor cGMP
RT      phosphodiesterase alpha- and beta-subunits, and identification of
RT      beta', a putative beta-subunit isozyme produced by alternative
RT      splicing of the beta-subunit gene.";
RT      FEBS Lett. 278:107-114 (1991)
CC      -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC      TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
CC      -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC      guanosine 5'-phosphate.
CC      -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC      BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC      -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC      FAMILY.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; X60664; CAA43072.1; -
CC      PIR; S13030; S13030.
CC      MGD; MGI:97524; Pde6a.
CC      InterPro; IPR003018; GAF.
CC      InterPro; IPR003607; ME_Pplase_Hdc.
CC      InterPro; IPR002073; PDEase.
CC      InterPro; IPR001230; Prenyl_site.
CC      Pfam; PF00233; PDEase; 1.
CC      Pfam; PF01590; GAF; 2.
CC      PRINTS; PR00387; PDIESTERASE1.
CC      SMART; SM00065; GAF; 2.
CC      SMART; SM00471; HDC; 1.
CC      PROSITE; PS00126; PDEASE_I; 1.
CC      Hydrolase; CGMP; Vision; Prenylation; Lipoprotein.
CC      INIT_MET 0
CC      LIPID 855 855 FARNESYL (BY SIMILARITY).
CC      SEQUENCE 858 AA; 99515 MW; E29AG26B23F7DDAO CRC64;
CC
CC      Query Match 18.8%; Score 183; DB 1; Length 858;
CC      Best Local Similarity 34.1%; Pred. No. 6.7e-08;
CC      Matches 43; Conservative 27; Mismatches 54; Indels 2; Gaps 2;
CC
CC      QY 54 KDRRFNDEIDKLTGYTKSLLCMPIRSSDGEIIGVAQAANKIPGAPFTEDEKVMOMYL 113
CC      DB 157 EDEHCFDVFVNLEYQTKNILASPIIMNGK-DVVAVIMAVNKIDE-PHFTKRDEILLKYL 214
CC      QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLKRCRC 173
CC      DB 215 NFVNLIMKVFHLSYLNHCETRRGQVLLWSGSKVFEELTDIERQFHKAFTVRFLNCDRY 274
CC      QY 174 SVLLLE 179
CC      DB 275 SVGLLD 280
CC
CC      RESULT 13
CC      CNRA_CANFA
CC      ID CNRA_CANFA STANDARD; PRT; 860 AA.
CC      AC Q28263; Q29470;
CC      DT 01-NOV-1997 (Rel. 35, Created)
CC      DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC      DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC      DE Rod CGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
CC      DE (EC 3.1.4.17) (GMP-PDE alpha).
CC      GN PDE6A OR PDEA.
CC      OS Canis familiaris (Dog).
CC      OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC      OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
CC      OX NCBI_TaxID=9615;
CC      [1]
CC      RN SEQUENCE FROM N.A.

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RC      TISSUE=Retina;
RX      MEDLINE=9631105; PubMed=8726673;
RA      Kommonen B., Kylma T., Cohen R.J., Penn J.S., Paulin L., Hurwitz M.,
RA      Hurwitz R.L.;
RT      "Elevation of cGMP with normal expression and activity of rod
RT      cGMP-PDE in photoreceptor degenerate labrador retrievers.";
RL      Ophthalmic Res. 28:19-28(1996).
RN      [2]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=98099662; PubMed=9233984;
RA      Wang W., Acland G.M., Aguirre G.D., Ray K.;
RT      "Cloning and characterization of the cDNA encoding the alpha-subunit
RT      of cGMP-phosphodiesterase in canine retinal rod photoreceptor cells.";
RL      Mol. Vision 2:3-3(1996).
RN      [3]
RN      SEQUENCE FROM N.A.
RC      STRAIN=Beagle X Briard; TISSUE=Retina;
RA      Veske A., Nilsson S.E.G., Gal A.;
RA      Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC      TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
CC      -1- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC      guanosine 5'-phosphate.
CC      -1- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC      BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC      -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC      FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Z68340; CAA92763.1; -;
DR      EMBL; U52868; AAB70037.1; -;
DR      EMBL; Y13282; CAA73731.1; -;
DR      InterPro; IPR003018; GAF.
DR      InterPro; IPR003607; ME_Pelase_HDC.
DR      InterPro; IPR002073; PDEase.
DR      InterPro; IPR001230; Prenyl_site.
DR      Pfam; PF00233; PDEase; 1.
DR      Pfam; PF01590; GAF; 2.
DR      PRINTS; PR00387; PDIESTERASE1.
DR      SMART; SM00065; GAF; 2.
DR      SMART; SM00471; HDC; 1.
DR      PROSITE; PS00126; PDEASE_I; 1.
KW      Hydrolase; cGMP; Vision; Prenylation; Lipoprotein.
FT      INIT_MET 0;
FT      LIPID 857 857 FARNESYL (BY SIMILARITY).
FT      CONFLICT 387 387 M -> L (IN REF. 2).
SQ      SEQUENCE 860 AA; 99557 MW; 5260B0BC579A25F7 CRC64;
Query Match 18.8%; Score 183; DB 1; Length 860;
Best Local Similarity 34.1%; Pred. No. 6.7e-08;
Matches 43; Conservative 27; Mismatches 54; Indels 2; Gaps 2;
Qy 54 KRRFNDEIDKLGKTKSLCLMPIRSSDGEIIGVAAOAIKIPGAPFTTEDEKVMOMYL 113
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
157 EDEHFCDFVDTLEYQPKNLASPIMGK-DVVAVIMAVNKVDE-PHFTKRDEEILLYL 214
Qy 114 PFCGIATISNAQLFAASRKEVERSFALLEVNDLFEETDLEKIVKIMHRAQTLLKCERC 173
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
215 NFANIMKVYHLSYLNHCETRRGQILLWSGSKVFEELTDIERQFKALYTVRAFLNCDRY 274
Qy 174 SVLLLE 179
Db : : : : :
275 SVGLLD 280
RESULT 14

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RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=91015387; PubMed=1977087;
RA Bowes C., Li T., Danciger M., Baxter L.C., Applebury M.L.,
Farber D.B.;
RT "Retinal degeneration in the rd mouse is caused by a defect in the
beta subunit of rod cGMP-phosphodiesterase.";
RL Nature 347:677-680(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=91130581; PubMed=1847109;
RA Baehr W., Champagne M.S., Lee A.K., Pittler S.J.;
RT "Complete cDNA sequences of mouse rod photoreceptor cGMP
phosphodiesterase alpha- and beta-subunits, and identification of
beta', a putative beta-subunit isozyme produced by alternative
splicing of the beta-subunit gene.";
RL FEBS Lett. 278:107-114(1991).
CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
guanosine 5'-phosphate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Beta';
are produced by alternative splicing.
CC -!- DISEASE: DEFECTS IN PDE6B ARE THE CAUSE OF RETINAL DEGENERATION.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY.
CC -----

Search completed: June 13, 2003, 15:47:44
Job time : 5.97722 secs

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EMBL: X55968; CAA39439.1; ALT_SEQ.
EMBL: X60133; CAA42719.1; -
PIR: S13121; S13121.
MGD: MGI:97525; Pde6b.
InterPro: IPR003018; GAF.
InterPro: IPR003607; ME_Pplase_Hdc.
InterPro: IPR002073; PDEase.
InterPro: IPR001230; Prenyl_site.
Pfam: PF00233; PDEase; 1.
Pfam: PF01590; GAF; 2.
PRINTS: PR00387; PDIESTERASE1.
SMART: SM00065; GAF; 2.
SMART: SM00471; Hdc; 1.
PROSITE: PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane;
KW Alternative splicing.
FT CHAIN 1 853 ROD CGMP-SPECIFIC 3',5'-CYCLIC
PROPEP 854 856 PHOSPHODIESTERASE BETA-SUBUNIT.
LIPID 853 853 REMOVED IN MATURE FORM (BY SIMILARITY).
VARSPPLIC 801 856 GERANYL-GERANYL (BY SIMILARITY).
CONFLICT 5 5 MISSING (IN ISOFORM 2).
CONFLICT 19 19 G -> E (IN REF. 2).
CONFLICT 49 50 S -> A (IN REF. 2).
CONFLICT 158 176 DV -> EL (IN REF. 2).
CONFLICT 176 176 T -> P (IN REF. 2).
CONFLICT 232 232 C -> L (IN REF. 2).
CONFLICT 236 236 R -> E (IN REF. 2).
CONFLICT 236 236 S -> G (IN REF. 2).
SEQUENCE 856 AA; 98501 MW; 3677704D0C7496D1 CRC64;

Query Match 17.9%; Score 175; DB 1; Length 856;
Best Local Similarity 33.68; Pred. No. 3.le-07;
Matches 45; Conservative 23; Mismatches 64; Indels 2; Gaps 2;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 15:05:11 ; Search time 3005 seconds
(without alignments)
11199.408 Million cell updates/sec

Title: US-09-663-542-2

Perfect score: 2078

Sequence: 1 ggtccgagatgctgaagcag.....actaataactcgaggcatgc 2078

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estopl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vit:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	528	25.4	648	10	BB595063
2	473	22.8	724	10	BB639291
3	216.8	10.4	459	12	BC554930
4	184.8	8.9	501	13	BF672945
5	177	8.5	689	14	BQ014209
6	166	8.0	472	17	AQ312583

7	155.4	7.5	884	9	AU079253
8	150.8	7.3	719	13	BI259167
9	150.8	7.3	941	13	BI259477
10	144.4	6.9	401	9	AI025081
11	142.8	6.9	744	14	BQ443199
12	141	6.8	644	13	BI255184
13	140.4	6.8	583	11	AK018833
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16	138.2	6.7	639	17	AG065785
17	137.8	6.6	1067	13	BM450793
18	135.8	6.5	875	14	BQ928876
19	135.6	6.5	561	10	BE107807
20	132.8	6.4	905	17	CNS01E4X
21	130.2	6.3	800	12	BG214519
22	128.8	6.2	747	12	BG342646
23	127.2	6.1	876	13	BI733977
24	126.8	6.1	790	12	BG206143
25	123.4	5.9	516	12	BG087768
26	121.8	5.9	636	14	BM950937
27	121.8	5.9	987	12	BG171485
28	121	5.8	747	12	BG215073
29	119.8	5.8	738	13	BI736696
30	119.6	5.8	632	13	BI285638
31	119.2	5.7	782	9	AU120086
32	118.2	5.7	579	13	BI706530
33	118	5.7	506	13	BI326168
34	117.6	5.7	621	13	BI395052
35	116.2	5.6	573	13	BI708657
36	116.2	5.6	600	13	BI708675
37	116	5.6	798	14	BQ720185
38	115.6	5.6	655	14	BQ572379
39	115.2	5.5	1004	14	BM923051
40	114.8	5.5	322	10	AW158676
41	114.8	5.5	607	10	AW640964
42	114.8	5.5	616	14	BQ400425
43	114.6	5.5	690	9	AI134280
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ALIGNMENTS

RESULT 1

BB595063

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BB595063 BB595063 648 bp mRNA linear EST 26-OCT-2001
musculus RIKEN full-length enriched, adult male corpus striatum Mus
cdna clone C030004B19 5', mRNA sequence.

BB595063 GI:16450156

BB595063

EST

house mouse

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 648)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,

Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda,

M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,

Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,

D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,

Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,

Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

On Nov 30, 2000 this sequence version replaced gi:11491665.

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

TITLE

JOURNAL

COMMENT

Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
 K., Fukuda, S., Harada, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for
 further details.

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

FEATURES

source

Location/Qualifiers
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 /strain="C57BL/6J"
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 /clone="C030004B19"
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 striatum"
 /sex="male"
 /tissue.type="corpus striatum"
 /dev_stage="adult"
 /lab_host="DH10B"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 185.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATCTCGAGTAAATTAATATCCCTCCCTCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pluescript KS(+) after bulk excision
 from Lambda FIC I. Cloning sites, 5' end: SalI; 3' end:
 BamHI"

BASE COUNT 181 a 146 c 154 g 167 t

ORIGIN

Query Match 25.4%; Score 528; DB 10; Length 648;
 Best Local Similarity 88.4%; Pred. No. 1e-141;
 Matches 573; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 267 GGTGGGCCCAAGCGATAAATAGATTCCTCAAGGAGCTCCATTTACTGAAGATGATCAA 326
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 Db 1 GGTGGGCCCAAGCGATAAATAGATTCCTCAAGGAGCTCCATTTACTGAAGATGATCAA 60

QY 327 AAAGTTATGCAGATGTATCTTCCATTTTGTGTAATCGCATATCTAAACGCTCAGCTCTTT 386
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 Db 61 AAAGTTATGCAGATGTATCTTCCGTTTCAAGTGAATCGCATATCTAAATGCTCAGCTCTTC 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 QY 387 GCTGCTCAAGGAAGAATATGAAAGAGCAGAGCTTTGCTAGAGGTGGTTAAATGACCTC 446
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 Db 121 GCTGCTCAAGGAAGAATACGAAAGAGCAGGCGCTTCTGGAGGTGGTCAATGACCTC 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 QY 447 TTTGAAGAACAGACTGACCTGGAGAAAATTTCAAGAAAATAATGCATCGGGCCCAACT 506
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 Db 181 TTTGAAGAACAGACTGATCTGAAAAGATTTGCAAGAAAATAATGCATCGGGCCCAACT 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 QY 507 CTGCTGAATGTGAGCGCTGTTCTGTTTACTCTAGAGGACATCGAATACCACTGCTGTG 566
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 Db 241 CTGCTGAATGTGAACGCTGTTCCGCTTACTTCTAGAGACATTTGAGTCCCACTGCTGTG 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 QY 567 AAATTTACCAATCCTTTTGAATTTGATGTCCTCCCAAGTGCAGTCTGCTGTGAGAACACT 626
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 Db 301 AAGTTTACCAATCCTTTTGAATTTGATGTCCTCCCAAGTGCAGGCTGATGCTGAGAACACT 360
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 QY 627 TTCAAGAAAGCATGCGAGAAATCATCATCTCCGACTGGCTAATAAATAACAGCAATGCT 686
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 Db 361 TTCAAGAGAGTGTGGAGAAATCGTCTTACTCTGACTGGCTGATAAACAACAGCATCGCT 420
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 QY 687 GAGCTGGTGTCTTCAACAGGCTTCCAGTGAACATCAGTGCCTACCAAGATCCGCGC 746
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 Db 421 GAGCTGGTGTCTTCAACAGGCTTCCAGTGAACATCAGTGCCTACCAAGATCCGCGC 480
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 QY 747 TTTGATGAGAGGAGCAGACAGATATCTGTTTTCACATAAGATCTGTTTGTGTCCT 806
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 Db 481 TTTGAGCTGAGGCTGACAGATATCTGTTTTCATATAAGATCTGTTTGTGTCCT 540
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 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
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RESULT 2

BB639291

LOCUS

BB639291

DEFINITION

musculus CDNA clone A630086N24 5', mRNA sequence.

ACCESSION

BB639291

VERSION

BB639291.1

KEYWORDS

EST

SOURCE

house mouse

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 724)

AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
 Hiramoto, K., Hori, F., Ito, M., Kawai, J., Konno, H., Kouda
 M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
 Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
 D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
 Muramatsu, M. and Hayashizaki, Y.

TITLE

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL

Unpublished (2001)

COMMENT

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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

	188 a	169 c	187 g	180 t	
ph		22.8%	Score 473;	DB 10;	Length 724;
l similarity		90.2%;	Pred. No. 1e-125;		
306;	Conservative	0;	Mismatches 55;	Indels 0;	Gaps 0;
43	ATCTTCCATTTTGTGGAATCGCCATATCTTAAGCGTCAGCTCTTTGCTGCTCAAGAAAG	402			
2	ATCTTCCGGTCTGTGGAATCGGCATATCTTAAGTCTCAGCTCTTCGCTGCTCAAGAAAG	61			
3	AATATGAAGAAGACAGAGCTTTGCTAGAGGTGGTTTAATGACCTCTTTGAAGAACACACTG	462			
52	AATACGAAGAAGACAGGGGCCCTGCTGGAGTGGTCAATGACCTCTTTGAAGACACACTG	121			
53	ACCTGGAGAAATTTGCAAGAAAATAATGCATGGGCCCAACTCTGCTGAAATGTGAGC	522			
222	ATCTGGAAAAGATTGTCAAGAAAATAATGCATGGGCCCAACTCTGCTGAAATGTGAAC	181			
223	GCTGTTCTCTTTTACTCTCTFAGAGGACATCGAATCACAGTGGTGAATTTACCAAAATCCT	582			
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Best Local Similarity 77.4%; Pred. No. 2.1e-51;
Matches 263; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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Db 1 TAATGACAGCGTGTGACCTTGAGCGGTGACCAACCGTGGGAGATCTCCAGACAGGTGG 60

QY 1750 CAGAAGCTTGTAAACAGTGTGCTTTCGAACAGGAGATCGGGAGAGATTAGAGCTCAAC 1809
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CTGAGTTGGTACAGTGTGCTTTCGAACAGGAGATCGGGAGAGATTAGAGCTCAAC 120

QY 1810 TCATCCCTTCAGCAATTTTGTATCGGAACCGGAAGGATGAATCGCTCGTTTCAACTGG 1869
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Db 121 TGACACCTTCAGCCATTTTGTATAGTGTGCTTTCGAACAGGATGAGCTTCTCGATTACAATTG 180

QY 1870 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1929
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240

QY 1930 TGAAGCCGATGCTAGATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1989
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 TTAAGCCTTATGTTGACTGTGACTGTGACTGTGACTGTGACTGTGACTGTGACTGTGACTG 300

QY 1990 AAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2029
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Db 301 AACAGTCTCATGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340

RESULT 4
B1672945
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

B1672945 501 bp mRNA linear EST 12-SEP-2001
ft39g12.y1 Gong zebrafish testis Danio rerio cDNA clone 5153110 5'
similar to TR:Q9WJ79 Q9WJ79 CG10231 PROTEIN. ; mRNA sequence.
B1672945
B1672945.1 GI:15588329
EST.
zebrafish.
Danio rerio.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
WashU zebrafish EST Project 1998
Unpublished (1998)
Other ESTs: ft39g12.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@wustl.edu
The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
Seq primer: T3 ET from Amersham
High quality sequence stop: 393.
Location/Qualifiers
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/clone="5153110"
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/sex="male"
/dev_stage="4-5 month"

FEATURES
source
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis (pooled); Vector: pBluescript SK-;
Site 1: XhoI; Site 2: EcoRI; Poly A+ RNA was isolated from
the testes of 31 male adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
```



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source
1. .689
/organism="Homo sapiens"
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/dev_stage="Adult"
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/Note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI CGAP EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CCS. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (GT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_LIB=UI-H-ED1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CGTCAGGCT"

BASE COUNT      182 a   126 c   125 g   253 t      3 others
ORIGIN

Query Match      8.5%; Score 177; DB 14; Length 689;
Best Local Similarity 58.8%; Pred. No. 9.6e-40;
Matches 322; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

QY 1362 CTGTGTCATGACCTCGACACGAGGGAACCAACATGCTTCCAAAGCTAAGAGTGCGCT 1421
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Db 684 CTAAGCCACGATNGGATCACCGTGGTGTGATRACTCTACATACACCGAAGTGAACAT 625

QY 1422 GCCCTGGCCCAACTCTATGGAACTCTGCTACCTGGAGCATACACATTTCAACACGCC 1481
   || || || || || || || || || || || || || || || || || || || || ||
Db 624 CCACTTGCCAGCTTTTACTG---CCATTCAATCATGGAACACCATCAITATGACCAGTGC 568

QY 1482 GTGATGATCCTTCAAAGTGAGGGTCACAAATATCTTTGCTAACCTGCTCTCCCAAGAAAT 1541
   || || || || || || || || || || || || || || || || || || || || ||
Db 567 GTATGATCTTATATAGTCAGGCATCAGATTTCTAGTGGCCTCTCCATTTGAAGAAAT 508

QY 1542 AGTGACCTTATGACGCTTTTGAAGCAGTCAATATTTGGCAACAGACCTCACGCTGTACTTT 1601
   || || || || || || || || || || || || || || || || || || || || ||
Db 507 AAGACCAGCTTGAATAATCAAGCAAGCTATTTTAGCTACAGACCTAGCACTGTACATT 448

QY 1602 GAGAGGAAGACTGAATCTTTTGAAGCTTCTAGTAAGAGAGATAGATTTGGAACATCAA 1661
   || || || || || || || || || || || || || || || || || || || || ||
Db 447 AAGAGCGGAGGAGAAATTTTGAAGCTTATAAGAAAAATCAATTTCAATTTGGAAGATCCT 388

QY 1662 AACCATCGTGATATATTTTCGATCAATGTTAATACAGACCTGTGACCTTTGGAGCGGTGACC 1721
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Db 387 CATCAAAAGGAGTGTGTTTGGCAATGCTGATGACGCTTGTGATCTTCTTGCATTTACA 328

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QY 1902 CAGGCACT 1909
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Db 147 GAGGTATT 140
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RESULT 6
AQ312583
LOCUS
DEFINITION
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ACCESSION
  AQ312583
VERSION
  AQ312583.1 GI:4044247
KEYWORDS
  GSS.
SOURCE
  human.
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 472)
  Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
  Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
  Use of human BAC End Sequences for Sequence-Ready Map Building
  Unpublished (1998)
  Other_GSSs: RPC111-95E23.TV
  Contact: Shaying Zhao, William Nierman, Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850
  Tel.: 301 838 0200
  Fax: 301 838 0208
  Email: hbeetigr.org
  Clones are derived from the human BAC library RPCI-11. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
  Research Genetics (info@resgen.com). BAC end search page:
  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
  Seq primer: SP6
  Class: BAC ends.
FEATURES
  Location/Qualifiers
    1..472
     /organism="Homo sapiens"
     /db_xref="GDB:7536214"
     /db_xref="taxon:9606"
     /clone="RPCI-11-95E23"
     /clone_lib="RPCI-11"
     /sex="Male"
     /cell_type="Lymphocytes"
     /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
     RPC11 Human Male BAC Library"
BASE COUNT      169 a   72 c   97 g   134 t
ORIGIN

Query Match      8.0%; Score 166; DB 17; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.2e-36;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAGATGCTGAAGCAGGCAAGAGACCTTTATTTCAGAAATGTCTCAGTGCCACACAGTGG 65
   || || || || || || || || || || || || || || || || || || || || ||
Db 33 GAGATGCTGAAGCAGGCAAGAGACCTTTATTTCAGAAATGTCTCAGTGCCACACAGTGG 92

QY 66 AAAAGGTGAAAATCACAAGACTGTGTCAAAATCTCTGGGGCCTCTTTGGCTGAAAAACAG 125
   || || || || || || || || || || || || || || || || || || || || ||
Db 93 AAAAGGTGAAAATCACAAGACTGTGTCAAAATCTCTGGGGCCTCTTTGGCTGAAAAACAG 152

QY 126 GAAAGACCAGGAGTTTCTTATACAGAGGCAACAAAAACAAGG 171
   || || || || || || || || || || || || || || || || || || || || ||
Db 153 GAAAGACCAGGAGTTTCTTATACAGAGGCAACAAAAACAAGG 198

RESULT 7
AU079253
LOCUS
DEFINITION
  AU079253 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-4049
  5', mRNA sequence.
ACCESSION
  AU079253
VERSION
  AU079253.1 GI:6084008
KEYWORDS
  EST.
SOURCE
  house mouse.
```


1320 ATTCTGACCGAGGTGGAATTTTTCAGGCGATGTTGGGATGCTGTCTCATGACCTCGAC 1379
184 TACCTCGAGACATCGAGATCTTTGCTTGTATTTCTGCTGATGTTGCTCATGACCTGGAC 243
1380 CACAGGGGACCAACAAATGCTTCCAAAGCTAAGAGTGGCTGCTCCCTGGCCCAACTCTAT 1439
244 CACAGGGGACCAACAACTCTTTCCAGGTGGCTCGAAATCTGTGCTGGCTGCGCTCTAC 303
1440 GGAACCTCTG---CTACCTTGGAGCATCACCACTTTCAACACCGCGTGATGCTCTCAA 1496
304 AGCTCTGAGGGTCCGTCATGAGAGGACCACTTTGCTCAGGCCATCGCCATCTCTCAAC 363
1497 AGTGAAGGTCACAATATTTGCTTAACCTGTCTCCAAAGGAATATAGTGAACCTTATGCGAG 1556
364 ACCACGGCTGCAACATCTTTGATCATCTTCTCCGGAAGGACTATCAGCGCATGCTGGAT 423
1557 CTTTGAACAGTCATATATGGAACAGACCTCACGCTGTACTTTGAGAGGAGAACTGAA 1616
424 CTGATCGGGACATCATCTTTGGCCACAGACCTGGCCCACTCTCCGCACTCTTCAAGGAC 483
1617 TTTCTTGAACCTGTCTAGTAAAGAGAAATACGATTTGGAACATCAAAAACCATCTGTATATA 1676
484 CTCAGAAGATGSC---TGAGTGGGCTAGGACCGGAACAAACAGCAGCACCACACTT 540
1677 TTTCTGATCAATGTTAATGACAGCCTGTGACCTTTGGAGCCGTGACCAAAACCGTGGGAGATC 1736
541 CTCCTCTGCTCTCATGACCTCTCTGACCTCTCTGACCAAGCAACCAAGGCTGGAAGACT 600
1737 TCCAGACAGGTGCGCAACTTGTAAACAGTGAAGTCTTTCGAACAAGAGATCGGGAGA 1794
601 ACGAAGAAGATCGCGAGCTGATCTACAAAGAATTTCTTCCAGGAGGAGACCTTGGAGA 658

RESULT 9

BI259477 941 bp mRNA linear EST 17-JUL-2001
LOCUS 602970109F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:510911 5',
DEFINITION mRNA sequence.

ACCESSION BI259477
VERSION BI259477.1 GI:14816850
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 941)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11265 row: b column: 04
High quality sequence stop: 771.
Location/Qualifiers

FEATURES

source
1..941
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:510911"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

BASE COUNT 228 a 283 c 229 g 201 t
ORIGIN
Query Match 7.3%; Score 150.8; DB 13; Length 941;
Best Local Similarity 54.0%; Pred. No. 4.7e-32;
Matches 355; Conservative 0; Mismatches 297; Indels 6; Gaps 2;
QY 1140 CTCGGATGTTTCATGGAGCTGGGATGGTACAGAAATTTAAAATTTGACTATGAGACACTG 1199
Db 4 CTGAGCATGCTGCAGGACATGAATTTTCATCAACAACACTACAAATTTGACTGCCCGACCTG 63
QY 1200 TGTAGTGGCTTTTTCAGACAGGAGAAACTATCGGATGGTCTTATACCAACTGGAGA 1259
Db 64 GCCCGGTTCTGTTTGTAGTGTGAAGAAGGGCTACCGGGATCCCGCTACCAACAACCTGGAT 123
QY 1260 CATGCGCTTCAACGTGTCTAGCTGATGTTCCGGCATGTTAAACCACTGCTGGTGTTCAGAC 1319
Db 124 CAGCGCTTTTCTGTCTCCCACTTCTGCTACCTGCTCTACAGAACCTGGAGCTCACCAAC 183
QY 1320 ATTCTGACCGAGGTGGAATTTTTCAGCGGTGATTTTGGGATGCTGTGTCATGACCTCGAC 1379
Db 184 TACCTCGAGGACATCGAGATCTTTGCTTGTATTTTCTGTCATGTCATGACCTCGAC 243
QY 1380 CACAGGGGACCAACAAATGCTTCCAAAGCTAAGAGTGGCTTGCCTTGGCCCAACTCTAT 1439
Db 244 CACAGAGGACCAACAACCTCTTTCCAGGTGGCTCGAAATCTGTGCTGGCTGCGCTCTAC 303
QY 1440 GGAACCTCTG---CTACCTTGGAGCATCACCACTTTCAACCAACCGGTGATGCTCTCAA 1496
Db 304 AGCTCTGAGGGTCCGTCATGAGAGGACCACTTTGCTCAGGCCATCGCCATCTCTCAAC 363
QY 1497 AGTGAAGGTCACAATATCTTTTGTAACTGCTCTCCAAAGGAATATAGTGAACCTTATGCGAG 1556
Db 364 ACCACGGCTGCAACATCTTTGATCATCTTCTCCGGAAGGACTATCAGCGCATGCTGGAT 423
QY 1557 CTTTGAAGCAGTCAATATATTTGGAACAGACCTCACGCTGTACTTTGAGAGGAGAACTGAA 1616
Db 424 CTGATCGGGACATCATCTTTGGCCACAGACCTGGCCCACTCTTCCAGGAGGAGACCTTCAAGGAC 483
QY 1617 TTTCTTGAACCTGTCTAGTAAAGAGAAATACGATTTGGAACATCAAAAACCATCTGTATATA 1676
Db 484 CTCAGAAGATGSC---TGAGTGGGCTACGACCGGAACCAACAGCAGCACCACACTT 540
QY 1677 TTTCTGATCAATGTTAATGACAGCCTGTGACCTTTGGAGCCGTGACCAAAACCGTGGGAGATC 1736
Db 541 CTCCTCTGCTCTCATGACCTCTCTGACCTCTCTGACCAAGCAACCAAGGCTTGGAGACT 600
QY 1737 TCCAGACAGGTGCGCAACTTGTAAACAGTGAAGTCTTTCGAACAAGAGATCGGGAGA 1794
Db 601 ACGAAGAAGATCGCGAGCTGATCTACAAAGAATTTCTTCCAGGAGGAGACCTTGGAGA 658

RESULT 10

AI025081 401 bp mRNA linear EST 27-AUG-1998
LOCUS ov40a11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639772
DEFINITION 3' similar to TR:Q28156 Q28156 CGMP-SPECIFIC PHOSPHODIESTERASE. ;
mRNA sequence.
ACCESSION AI025081
VERSION AI025081.1 GI:3240694
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 401)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaudo

Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/burp/image/image.html
Insert length: 648 Std Error: 0.00
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 370.

FEATURES

Location/Qualifiers
1. .401
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1639772"
/sex="male"
/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5',
TGTTCACCATCTGAAGTGGAGCGCGGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 123 a 89 c 63 g 126 t
ORIGIN

Query Match 6.9%; Score 144.4; DB 9; Length 401;

Best Local Similarity 96.1%; Pred. No. 2e-30;

Matches 148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 409 AAGAGACGAGCTTGGTAGAGTGGTTAATGACCTTTTGAAGACAGACTGACCTGG 468

Db 221 AAAGCTGCTGGTTTGGTAGAGTGGTTAATGACCTTTTGAAGACAGACTGACCTGG 162

QY 469 AGAAATGTCAGAAAATAATGCATCGGCGCCCAACTCTGCTGAATGTGAGCGCTGTT 528

Db 161 AGAAATGTCAGAAAATAATGCATCGGCGCCCAACTCTGCTGAATGTGAGCGCTGTT 102

QY 529 CTCTTTTACTCTCCTAGAGGACATCGAATCACCAGT 562

Db 101 CTCTTTTACTCTCCTAGAGGACATCGAATCACCAGT 68

RESULT 11

BQ443199

LOCUS

DEFINITION

UI-M-EV0-bxg-k-19-0-UI.r1 NIH_BMAP_EV0 Mus musculus cDNA clone

IMAGE:5707914 5', mRNA sequence.

BQ443199

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

744 bp mRNA linear EST 29-MAY-2002
UI-M-EV0-bxg-k-19-0-UI.r1 NIH_BMAP_EV0 Mus musculus cDNA clone
IMAGE:5707914 5', mRNA sequence.
BQ443199
BQ443199.1 GI:21246311
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 744)
NIH-MGC <http://imgc.ncbi.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

FEATURES

Location/Qualifiers
1. .744

/organism="Mus musculus"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:5707914"

/clone_lib="NIH_BMAP_EV0"

/tissue_type="whole brain"

/dev_stage="embryo 15.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
, is GTGGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP); 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 183 a 227 c 156 g 175 t 3 others

ORIGIN

Query Match 6.9%; Score 142.8; DB 14; Length 744;

Best Local Similarity 53.1%; Pred. No. 8.6e-30;

Matches 347; Conservative 0; Mismatches 300; Indels 6; Gaps 2;

QY 1107 TCTCTCGAGCTTGATGCCATGATCACAGCTGCTCTCCGATGTTTCAGAGTGGGGATG 1166

Db 88 TCTCTCGAGCTTGATGCCATGATCACAGCTGCTCTCCGATGTTTCAGAGTGGGGATG 147

QY 1167 GTACAGAAATTTAAATTCAGTATGAGACACTGTGTAGTGGCTTTTGACAGTGAAGAA 1226

Db 148 ATCAATATCTACAAATTCAGTATGAGTGGCTTTTGACAGTGAAGAA 207

QY 1227 AACTATCGGATGTTCTATACCACTGGAGACATGCTTCAACCTGTGTACAGTGTATG 1286

Db 208 GGCTACCGGGATCCACCTTACCACACTGGATCGACGCTCTCTCTCTCATTTTGC 267

QY 1287 TTCCGGATCTTACCACTGCTGGGTTTCAAGACATTTCTGACCGAGTGGAAATTTAGCG 1346

Db 268 TACCTGCTCTACAAGAACTGGAGCTCTCCAACTACCTCGAGGACATCGAGATCTTTGCA 327

QY 1347 GTGATTGGGATGCTGTGTCATGACCTCGACCAGGGGACCAACATGCCTTCCAA 1406

Db 328 TTGTTTATTTCTTGGCATGTGTATGACCTGGGACAGAGGACCAAACTCCTTCCAG 387

QY 1407 GCTAAGAGTGGCTTGCCTCGCCCAACTCTATGGAACCTCTG---CTACCTTTGAGCAT 1463

Db 388 GTGGCTCGAATCTGTGCTGGCCCACTCTACAGCTCAGAGGGCTCTCTCATCGAGAGG 447

QY 1464 CACCATTTCAACACGCGCTGATGATCTTCAAGTGGGGTCAATAATCTTTGTGTAAC 1523

Db 448 CACCATTTTGCCTCAAGCCATTCATCTCTCAACACCGGCTGCAATATCTTTGACCAC 507

QY 1524 CTTGCTCTCAAGGAATATAGTACCTTATGCAGCTTTTCAACAGCAGTCAATATGGCAAC 1583

Db 508 TTCTCTCGGAAGGACTATCAGCGCATGCTGGACCTGTATGAGGACATCATCTTTGGCTACA 567

QY 1584 GACCTCACCTCTACTTTTGAGAGGAGAACTGAATTTTGAACCTTGTTCAGTAGAAGAGAA 1643

Db 568 GACCTGGCACACCACTCTCGCATCTTCAGGACCTCCCAAGATGCG---TGAAGTGGGT 624

QY 1644 TAGGATTGGAACATCAAAACCATCGTGATATATTTTCGATCAATGTTAATGACAGCTGT 1703

Db 625 TATGACCGAACAACAGGCAACACAGGCTTCTTCTGTGCTCTCTCATGACCTCTCTGT 684

Db	302	GAATCTGTGCTGGCGCTCTACAGCTCTGAGGCGCTCGGTATCATGGAGGACCACCTT	361
QY	1472	CAACCACCGCGTGATGATCTTCAAAAGTGGAGGCTCAACAATATATTTTCTAACTGTGCCTC	1531
Db	362	TGCTCAGGCCATCGCCATCCTCAACACCCACGCGCTGCAACATCTTTTGATCATTTCTCCCG	421
QY	1532	CAGGAATATATGACCTTATGACAGCTTTTGAAGCAGTCAATATTTGGCAACAGACCTCAC	1591
Db	422	GAAGGACTATCAGCGCATGCTGATCTGATCGCGGACATCATCTTGCCACAGACCTGGC	481
QY	1592	GCCTGTACTTTGAGAGGAGAACTCAATCTTTGAACCTTGTCAGTAAAGGAGAAATACCATTC	1651
Db	482	CCACCATCTCCGCATCTTCAAGGACCTCCAGAAGATGG---CTGAGTGGGCTACGACCG	538
QY	1652	GAACATCAAAAACCATCGTGCATATATTTTCATCAATCTTAAATGACAGCCTGTGACCTTGG	1711
Db	539	ARACACAGCAGCACCAGACATCTCTCTCTCCCTCATGACCTCTCTGTGACCTCTC	598
QY	1712	AGCCGTGACCAACCGTGGGAGATCTCCAGACAGGTGGCGAAGACT	1756
Db	599	TGACCAGACCAAGCGCTGGAAGACTACGAGAAAGATCGCGGAGCT	643
RESULT 13			
LOCUS	AK018833		
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700008G06:cytochrome c, testis, full insert sequence.		
ACCESSION	AK018833	583 bp	mrna
VERSION	AK018833.1	GI:12858775	linear
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library		
	clone:1700008G06.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
REFERENCE	1		
AUTHORS	Carninci,P. and Hayashizaki,Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	9279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries: for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	2049374		
PUBMED	2049374		
REFERENCE	3		
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Hatada,A., Yamamoto,R., Matsumoto,H., Sakauechi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Fumanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Sakakura,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,J., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,		

Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851

REFERENCE

5 (bases 1 to 583)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Soabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGAGCGCGCAATTAATTCAGTAAATTAATCCCGCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI, 3' end: SstI. Host: SOLR.

FEATURES

Location/Qualifiers

1..583

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="PANTOM.DB:1700008G06"

/db_xref="MGD.MGI:1899654"

/db_xref="taxon:10090"

/clone="1700008G06"

/sex="male"

/tissue_type="testis"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

1..583

/gene="Cycyt"

129..446

/gene="Cycyt"

/note="cytochrome c, testis"

data source:MGD, source key:MG1:88579, evidence:ISS

putative"

gene

CDS

/codon_start=1
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/db_xref="MGD.MGI:88579"
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PGFSYTDANKNGKVIWSEETLMLEYLENPKYIPGKTMIFAGIKKXSEREDLTKYLKQA
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558..563
/gene="Cycyt"
/note="putative"
583
/gene="Cycyt"
/note="putative"
BASE COUNT 194 a 100 c 135 g 154 t
ORIGIN

Query Match 6.8%; Score 140.4; DB 11; Length 583;
Best Local Similarity 90.4%; Pred. No. 3.7e-29;
Matches 150; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 6 GAGATGCTGAAGCAGGCAAGAGACCTTTATTTCAGAAATGTCTCAGTGCACACAGTGG 65
|||||
DB 133 GAGATGCTGAAGCAGGCAAGAGATCTTTGTTTCAGAAATGTCTCAGTGCACACAGTGG 192
|||||
QY 66 AAAAGGTGAAATACACAAAGACTGTGCTCAAAATCTCTGGGGCTCTTTTGGCTGAAAAACAG 125
|||||
DB 193 AAAAGGCGGCAACACAAAGACAGTCCAAATCTCTGGGGCTCTTTTGGTGAAGACAG. 252
|||||
QY 126 GAAAGACACAGGATTTCTTATACAGAGCAACAAACAAAAGG 171
|||||
DB 253 GACAAGCACCAGGATTTCTTACAGGATGCAAAACAAAGG 298
|||||

RESULT 14

AK005582

LOCUS

DEFINITION

Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700001D24:cytochrome c, testis, full insert sequence.

ACCESSION

AK005582

VERSION

AK005582.1 GI:12838235

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone:lib:RIKEN full-length enriched mouse cDNA library

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Carninci, P. and Hayashizaki, Y.

TITLE

High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCE

2

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE

20499374

PUBMED

11042159

REFERENCE

3

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL

Genome Res. 10 (11), 1757-1771 (2000)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 10:41:07 ; Search time 489 seconds

(without alignments)
9569.842 Million cell updates/sec

Title: US-09-663-542-2

Perfect score: 2078

Sequence: 1 ggtccgagatgctgaagcag.....actaataactcgagcgatgc 2078

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2078	100.0	2078	22	AAF62311 Human cyclic nucle
2	2056.4	99.0	3507	22	AAH46709 Human type 11 phos
3	1891.8	91.0	4476	22	AAH46708 Human type 11 phos
4	1734.8	83.5	2994	22	AAH78232 Nucleotide sequenc
5	1684	81.0	3492	22	AAH46710 Rat type 11 phosph
6	1551.4	74.7	4170	22	AAH46742 Rat type 11 phosph
7	1503.8	72.4	1784	21	AAH49972 Human cyclic nucle
8	1421.8	68.4	2513	21	AAH78223 Nucleotide sequenc
9	1045.6	50.3	1982	21	AAA49973 Human cyclic nucle

10	388.8	18.7	.426	24	AAZ28571 Human PDE-like enz
11	356.6	17.2	2499	21	AAA39042 Human cGMP phospho
12	356.6	17.2	2499	21	AAZ95234 Human phosphodiester
13	356.6	17.2	2499	22	AAF95963 Human phosphodiester
14	356.6	17.2	2645	16	AAQ79715 Cyclic guanosine m
15	356.6	17.2	2645	20	AAZ99393 Human cGMP-binding
16	355	17.1	2499	21	AAZ95233 Human phosphodiester
17	355	17.1	3381	21	AAA14957 DNA encoding a PDE
18	345.2	16.6	1982	16	AAQ79705 Cyclic guanosine m
19	345.2	16.6	1982	19	AAV05066 Bovine phosphodies
20	345.2	16.6	1982	20	AAZ99383 Human cGMP-PDE cDNA
21	343.6	16.5	4426	19	AAV09064 Bovine cGMP-bindin
22	343.6	16.5	4474	20	AAZ99381 Bovine cGMP-bindin
23	340.8	16.4	4474	16	AAQ79703 Cyclic guanosine m
24	339.4	16.3	3855	23	ABL30105 Drosophila melanog
25	224.2	10.8	3699	23	ABL13737 Drosophila melanog
26	219.2	10.5	2406	21	AAQ09590 Human phosphodiester
27	219.2	10.5	2554	21	AAZ36963 DNA encoding a hum
28	219.2	10.5	2798	21	AAZ36964 DNA encoding a hum
29	219.2	10.5	3631	22	ABA03665 Human PDE10A cDNA
30	219.2	10.5	4576	21	AAQ09589 Human phosphodiester
31	217.6	10.5	2298	20	AAZ36710 Human phosphodiester
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36	217.6	10.5	4389	20	AAZ36711 Human phosphodiester
37	217.6	10.5	4389	22	AAZ36711 Human phosphodiester
38	216.6	10.4	3789	16	AAQ83977 Cyclic-GMP stimula
39	216.6	10.4	3789	18	AAZ67223 cGMP-PDE cDNA seque
40	216.6	10.4	3789	18	AAZ67223 Coding sequence fo
41	216.6	10.4	3789	19	AAV48204 Cyclic-GMP-stimula
42	216.6	10.4	3789	19	AAV48204 Bovine brain cGMP-P
43	216.6	10.4	3789	19	AAV48204 cGMP-PDE cDNA isola
44	216.6	10.4	3789	21	AAZ90380 Bovine brain cGMP-P
45	216.6	10.4	4131	13	AAQ30180 cGMP-PDE cDNA clone

ALIGNMENTS

RESULT 1

AAF62311

ID AAF62311 standard; cDNA; 2078 BP.

XX

AC AAF62311;

XX

DT 06-JUN-2001 (first entry)

XX

DE Human cyclic nucleotide phosphodiesterase PDE XV coding sequence.

XX

KW Human; cyclic nucleotide phosphodiesterase; PDE XV; sexual dysfunction;

KW cardiovascular disease; gastrointestinal disorder; corpus cavernosum;

KW kidney; liver; skeletal muscle; testis prostate; spleen; ss.

XX Homo sapiens.

XX Key.

FT CDS

FT Location/Qualifiers

FT 9..2063

FT /*tag= a

FT /product= "PDE XV"

XX EP1085089-A2.

XX

PD 21-MAR-2001.

XX

PF 14-SEP-2000; 2000EP-0307981.

XX

PR 17-SEP-1999; 99GB-0022124.

XX

PA (PF12) PFIZER LTD.

XX (PF12) PFIZER INC.

XX

QY 409 AAAGAAGCAGAGCTTTGCTAGAGGTGGTTAATGACCTCTTTTGAAGAACAGACTGACCTGG 468
DB 1469 AAAGAAGCAGAGCTTTGCTAGAGGTGGTTAATGACCTCTTTTGAAGAACAGACTGACCTGG 1528
QY 469 AGAAAATGTCAGAAAATATATGCAATCGGCGCCCAACTCTGCTGAATCTGAGCCCTGTT 528
DB 1529 AGAAAATGTCAGAAAATATATGCAATCGGCGCCCAACTCTGCTGAATCTGAGCCCTGTT 1588
QY 529 CTGTTTACTCTAGAGGACATCGAATCACCAGTGGTGAATTTTACCAGTCTTGAAT 588
DB 1589 CTGTTTACTCTAGAGGACATCGAATCACCAGTGGTGAATTTTACCAGTCTTGAAT 1648
QY 589 TGATGTCCCAAGTGCAGTGTGATGCTGAGAACAGTGTTCAGAAAGAGCATGGAAGAT 648
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DB 2009 ATGATCAAGTGAAGTCTCTGGGCCAAGCAGTCTGTGCTCTTGTATGCTGATATACC 2068
QY 1009 ATGCAACATGTTCAAAAGCTGAAGTGTGACAAGTTTAAAGCAGCCCAACATCCCTCTGGTGT 1068
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QY 1189 ATGACAGACTGTAGTGGCTTTTGCACAGTGAAGAAACATATCGGATGGTTCATACC 1248
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DB 3029 AGTGGGAAGAGCTACACCAAAACGACTGCTGGCTTCAACTGCCCTCATCTCTCCCTG 3088
QY 2029 CCAGTGTATTGTAGCCAAAGGAGACAGGAATAA 2063
DB 3089 CCAGTGTATTGTAGCCAAAGGAGACAGGAATAA 3123

RESULT 4
AAH78232
ID AAH78232 standard; DNA; 2994 BP.
XX
AC AAH78232;
XX
DT 26-NOV-2001 (first entry)
XX
DE Nucleotide sequence of a human phosphodiesterase polypeptide.
XX
KW Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension;
KW nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism;
KW osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis;
KW Parkinson's disease; dementia; infectious disease; malignant tumour; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT 631..2361
FT /*tag= a
FT /product= "phosphodiesterase"
XX
PN WO200166716-A1.
XX
PD 13-SEP-2001.
XX
PF 06-MAR-2001; 2001WO-JP01720.
XX
PR 07-MAR-2000; 2000JP-0061464.
XX
PR 10-JUL-2000; 2000JP-0208610.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX

AC AAH46710;
XX 19-SEP-2001 (first entry)
XX Rat type 11 phosphodiesterase coding sequence SEQ ID NO: 5.
DE Rat: type 11 phosphodiesterase; pDE11; signal transduction;
XX selective inhibition; ds.
KW Rattus sp.
XX OS
XX FH Location/Qualifiers
XX CDS 241..2298
FT /*tag= a
FT /product= "pDE11"
XX
XX WO200146436-A1.
XX 28-JUN-2001.
XX
XX 22-DEC-2000; 2000WO-JP09118.
XX
XX 22-DEC-1999; 99JP-0364866.
PR 01-JUN-2000; 2000JP-0163875.
XX
XX (TANA) TANABE SEIYAKU CO.
XX
XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX WPI: 2001-418074/44.
DR P-PSDB; AAG62679.
XX
XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy
XX
XX Claim 7; Page 51-55; 77pp; Japanese.
XX
XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (pDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a coding sequence of the invention.
XX
XX Sequence 3492 BP; 963 A; 792 C; 865 G; 872 T; 0 other;
SQ
Query Match 81.0%; Score 1684; DB 22; Length 3492;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 235; Indels 3; Gaps 1;
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DB 238 GAGATGCTGAGCAGGCGAAGAGATTTTCATTCAGAAATGTGCGCAGTGCACACAGTGG 297
QY 66 AAAAAGGTGAAATCACAGACTGTGCCAAATCTCTGGGCTCTTTGGCTCAAAAACAG 125
DB 298 AGAAAGGTGGAGCAGCAGGCGGCAAAATCTCTGGGCTCTTTGGCGGAAAGACTG 357
QY 126 GAAAAGCACCAGGATTTCTTATACAGGCGAAGCAAAAACAAAGGATCGACGATTCAT 185
DB 358 GACAAGCACCAGGATTTCTTATACAGGATGCAAAACAGACAAAGGACCGAGATTCAT 417
QY 186 GATGAATTCGCAAGCTGACTGGATACAGACAAATCATTTATGTGATGCTATCCGA 245
DB 418 GATGAATTCGCAAGCTGACTGGATACAGACAAATCATTTATGTGATGCTATCCGG 477
QY 246 AGCAGTGTGATGATGATTTGGTGTGGCCCAAGCGATTAATTAAGATTCCTGAAGGACT 305
DB 478 AACAGTGACGGTGAGATTCGGTGTGGCCCAAGCGGATAAATGAAGTTCCCTGAGGGTGT 537

QY 306 CCATTTACTGAAGATGATGAAAAAGTTATGAGATGATGATCTTCCATTTTGTGAATCC 365
DB 538 CCATTTACAGAAGACGACGAAAAAGTTATGAGATGATGATCTTCCATTTTGTGGATCCG 597
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QY 546 GACATCGAATCACCAGTGTGTAATTTTACCAAACTCTTTGAATGATGTCTCCCAAGTGC 605
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DB 838 AGTGGGACGGGAGAACAGTTTCAAGAAAGTGTGGAGAACTCATCTTACTCCGACTGG 897
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QY 846 GTGTTAAACAGACTTGTGGGAAACCTTTTGTATGATGACAGATCAACAGCTTTTTTGGGCT 905
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QY 906 TTTGTCATCTTTTGTGGACTTGGCATCAACACACAAATATGATATCATCAAGTGAAGAAG 965
DB 1138 TTTGTCATCTTTTGTGGCTTGGTATTAACAACAGCATTTATGATGACCAAGTGAAGAAG 1197
QY 966 TCCTGGGCAACAGCTCTGTGCTCTGATGTGCTATCATACCATGCAACATGTTTCAAAA 1025
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QY 1086 GACATTCATTTGTGACTTTTCTCTGACGTTGATGCGATGATGATGATGATGATGATG 1145
DB 1318 GACATTCATTTGTGACTTTTCCCTGATGTTGATGCTGATGATGATGATGATGATGATG 1377
QY 1146 ATGTTCTGAGCTGGGATGTACAGAAATTTTAAATTTGATGATGATGATGATGATGATG 1205
DB 1378 ATGTTCTGAGCTGGGATGTACAGAAATTTTAAATTTGATGATGATGATGATGATGATG 1437
QY 1206 TGGCTTTTGAAGTGAAGGAAATTCATCGGATGTTTCTATACCAACTTGGAGATGCC 1265
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QY 1266 TTCAACGTGTGTGACTGATGTTCCGATGTTAAACCATGCTGCTGGGTTTCAAGACATTCG 1325
DB 1498 TTCAACGTGTGCTGCTGATGTTTCCCATGCTTAACCTACTGCTGGGTTTCAAGAGATTCG 1557
QY 1326 ACCGAGGTGGAATTTTACGCTGATTTAGCGGTGATTTAGCGGTGATTTAGCGGTGATTT 1385
DB 1558 ACCGAGGTGGAATTTTACGCTGATTTAGCGGTGATTTAGCGGTGATTTAGCGGTGATTT 1617
QY 1386 GGAACCAACAATGCTTCCAAAGCTTAAGAGTGGCTCTGCTGCTGGCCCAACTCTTATGGAACC 1445

Db	1679	TATCTGGCTTTTCAATAAGATCTGTTCTCTGTCCTTATTTGGAACAGCAACACCAAA	1738
Qy	829	TAATTTGGAGTGGCTCAACTGTTAAACACACATGATGGGAACCTTTTCATGATGAGATC	888
Db	1739	TAATAGGGTGGCTCAAGTGTGAACAGACATCGATGGGAACCTTTTCATGATGCTGACC	1798
Qy	889	AACGACTTTTGGAGCTTTTGTGTCATCTTTTGTGGACTTGGCATCAACACACAATATGT	948
Db	1799	AAAGCTTTTGGAGCTTTTGTCTATCTTTTGTGGCTTGGTATTAACACACGATATGT	1858
Qy	949	ATGATCAATGAAGAAGTCTCGGGCCAAAGCAGCTCTGTGGCTTGTGATGTGTATCATACC	1008
Db	1859	ATGACCAAGTGAAGAAGTCTCGGGCCAAAGCAGCTCTGTGGCTTGTGATGTGTCTTACC	1918
Qy	1009	ATGCAACATGTTTCAAAAGCTGAAGTTGACAGTTTAAAGCAGCCCAACATCCTCTGGTGT	1068
Db	1919	ACGCCACGTGTTCCAAAGCTGAAGTTGACAGTTTAAAGCAGCCCAACATCCTCGGTGT	1978
Qy	1069	CAGAACTTGGCATCGATGACATTCATTTTGTGATGACTTTTCTCGACGTTGATGCGATGA	1128
Db	1979	CGAACTGGCCATCGATGACATTCATTTTGTGATGACTTTTCTCGATGTTGATGCCATGA	2038
Qy	1129	TCACAGCTGCTCTCGGATGTTTATGAGCTGGGATGGTACAGAAATTTAAATTTGACT	1189
Db	2039	TCACAGCGCTCTACGGATGTTTATGAGCTGGGATGGTACAGAAATTTAAATTCGACT	2098
Qy	1189	ATGACACACTGTGTAGTGGCTTTTGACAGTGCAGAGCAAGAAACTATCGGATGTTCTATACC	1248
Db	2099	ATGAGACCTGTGTAGTGGCTTTTGACAGTGCAGAGTAAAGAAACTATCGGATGTTCTTACC	2158
Qy	1249	ACAACTGGAGACATGCTTCAACGTGTGTGACGTGATGTCGAGTGTAAACCACTGCTG	1308
Db	2159	ACAACTGGAGACATGCTTCAACGTGTGCCAGCTGATGTTGCCATGCTAATCTACTGCTG	2218
Qy	1309	GGTTTCAAGACATTCGACCGAGTGGAAATTTTAGCGGTGATTTGGGATGCTGCTGTCTC	1368
Db	2219	GGTTTCAAGACATTCGACCGAGTGGAAATTTTAGCGGTGATTTGGGATGCTGCTGTCTC	2278
Qy	1369	ATGACCTCGACACAGGGGAACCAACATGCTTCCAGCTTAAGAGTGGCTCTGCCCCGG	1428
Db	2279	ATGACCTCGACACAGGGGAACCAACATGCTTCCAGCTTAAGAGTGAATCTGACCTGG	2338
Qy	1429	CCCAACTATGAACTCTGCTACTCTGGAGCATCACCATTCAACACGCGCGTATGA	1488
Db	2339	CCCACTCTATGGAGCTTCAAGGACCTTAGAGCATCACCATTAAACACGCGGTATGA	2398
Qy	1489	TCCTTCAAGTGAAGGTGCACATATCTTTTGTCTTAACCTGTCTCCAAAGGAATATAGTGACC	1548
Db	2399	TCCTTCAAGTGAAGGTGCACATATCTTTTGTCTTAACCTGTCTCCAAAGGAATACAGCGACC	2458
Qy	1549	TTATGACGCTTTTGAAGCAGTCAATATTGGCAACAGACCTACGCTGTACTTTGAGAGGA	1608
Db	2459	TCATGAGCTCTGTAAGCAGTGCATACATAGCCACTGACCTACGCTGTACTTCGAGAGAA	2518
Qy	1609	GAACTGAATCTTTGAACTTGTCAAGTAAAGAGATACGATTGGAAACATCAAAACCATC	1668
Db	2519	GAACTGAGTCTTTCAGCTTGTTCAGTAAAGAGCTATGATTTGGAGCATCACAAGTCACC	2578
Qy	1669	GTGATATATTTTCGATCAATGTTAATGACAGCCTGTGACCTTGGAGCCGTGACCAACCGT	1728
Db	2579	GGATGTGTGTTTCGATCAATGTTAATGACAGCTGTGTGACCTTGGAGCCGTGACCAACCGT	2638
Qy	1729	GGAGATCTCCAGAGTGGCAGAACTTGTAAACAGTCAAGTCTTCTCAACAGAGATC	1788
Db	2639	GGAGATCTCCAGAGTGGCTGAATTTGATCACCAGCGAGTCTTCAACAGAGAGATC	2698
Qy	1789	GGAGAGATTTAGAGTCAAACTCACTCTCTTACAGCAATTTTTCATCGGAACCGGAAGATG	1848
Db	2699	GGAGAGTTCGAATCAAGCTCACCCCTCTGCTATTTTTCACCGGAACCGGAAGATG	2758
Qy	1849	ACTCGCTCGGTGGAACTGGAGTGGATGATAGCATCTGCATGCTTGTATACGGCAC	1908
Db		TT	
Db	2759	AGTGCCTCGGCTGCAACTGGAGTGGATTTGACAGCATCTGCATGCTTGTATCAGGCT	2818
Qy	1909	TGGTGAAGTCAACCTGAAGCTGAAGCTGAAGCTAGATTCAAGTACATAAACAAGAGTA	1968
Db	2819	TGGTGAAGTCAATCAAACTGAAGCTGAAGCTAGTGGAGTCTAGTGGCCCAACCCAGGA	2878
Qy	1969	AGTGGGAAGACTACACCAAAACGACTGCTGGCCCTCAACTGCCT---CATCCTCTCTCC	2025
Db	2879	AGTGGGAAGACTGACCAAAAGACTACAGTCTCTGCTGCCTCCCAAGTCCCTTCCA	2938
Qy	2026	CTGCCAGTGTATGTTAGTCCCAAGGAGACAGAACTAATACTCGAGCATGC	2078
Db	2939	GTCCAGCCAGCGGTGGCCGAGAGAGACTGTAACACCAACCCAGAGCTGC	2991
RESULT 7			
AA449972	ID	AAA49972 standard; cDNA; 1784 BP.	
XX	AC	AAA49972;	
XX	DT	10-OCT-2000 (first entry)	
XX	DE	Human cyclic nucleotide phosphodiesterase HSPDE10A1 cDNA.	
XX	KW	Cyclic nucleotide phosphodiesterase; HSPDE10A1; human; cancer;	
XX	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
XX	FT	151..1623	
XX	FT	/*tag= a	
XX	PN	WO200040733-A1.	
XX	PD	13-JUL-2000.	
XX	PF	07-JAN-2000; 2000WO-US00371.	
XX	PR	07-JAN-1999; 99US-0226741.	
XX	PA	(INCY-) INCYTE PHARM INC.	
XX	PI	Phillips SC, Lanfear J, Fawcett L, Bandman O, Harrow I;	
XX	DR	WPI; 2000-452539/39.	
XX	DR	P-PSDB; AAY95521.	
XX	PT	New human cyclic nucleotide phosphodiesterases, referred as HSPDE10A1	
XX	PT	and HSPDE10A2, useful for treating and preventing cancer and immune	
XX	PS	disorders -	
XX	PS	Claim 4; Page 85; 96pp; English.	
XX	CC	The present sequence is that of cDNA encoding HSPDE10A1 (see	
XX	CC	AAV95521), a novel human cyclic nucleotide phosphodiesterase. The	
XX	CC	cDNA was initially identified in Incyte Clone 826776 from the	
XX	CC	prostate cDNA library PROSTUT04 using BLAST analysis and human	
XX	CC	phosphodiesterase 5 as query. Full-length cDNA sequences of	
XX	CC	HSPDE10A1 were obtained from a human skeletal muscle library using	
XX	CC	the complete cDNA insert of Incyte Clone 826776 as probe. The	
XX	CC	invention provides expression vectors, host cells, antibodies,	
XX	CC	agonists and antagonists, as well as methods for diagnosing,	
XX	CC	treating or preventing disorders associated with expression of	
XX	CC	HSPDE10A1, especially cancer and immune disorders. A fragment of	
XX	CC	the present sequence from about nucleotide 1168 to nucleotide 1212	
XX	CC	is useful in hybridisation or amplification technologies to	
XX	CC	distinguish HSPDE10A1 sequences from related sequences.	
XX	SQ	Sequence 1784 BP; 495 A; 400 C; 417 G; 472 T; 0 other;	
Query Match 72.4%; Score 1503.8; DB 21; Length 1784;			

Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	557	ACCAGTGGTGAATTTACCAATCTTTGAATGTGTCGCCAAAGTGCAGTGCATGTC	616
Db	117	ACAGTGGTGAATTTACCAATCTTTGAATGTGTCGCCAAAGTGCAGTGCATGTC	176
QY	617	TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA	676
Db	177	TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA	236
QY	677	CAGCATTTGCTGAGCTGGTGTTCACAGGCGCTCCAGTGAACATCATGATGCCTACCA	736
Db	237	CAGCATTTGCTGAGCTGGTGTTCACAGGCGCTCCAGTGAACATCATGATGCCTACCA	296
QY	737	GGATCCGGCTTTTGATGAGAGGAGACAGATATCTGTTTTCACATAAAGATCTGTTCT	796
Db	297	GGATCCGGCTTTTGATGAGAGGAGACAGATATCTGTTTTCACATAAAGATCTGTTCT	356
QY	797	TTGTGTCCTATTTGGAATAGCAACACCAATAATTTGAGTGGCTCAAGTGTAAACAG	856
Db	357	TTGTGTCCTATTTGGAATAGCAACACCAATAATTTGAGTGGCTCAAGTGTAAACAG	416
QY	857	ACTTGATGGGAACCTTTTGATGATGCAGATCAACGACTTTTGGAGCTTTTGTCACTTT	916
Db	417	ACTTGATGGGAACCTTTTGATGATGCAGATCAACGACTTTTGGAGCTTTTGTCACTTT	476
QY	917	TTGTGGACTTGGCATCAACACACAAATTTATGATCAAGTGAAGAAGTCTCTGGGCCAA	976
Db	477	TTGTGGACTTGGCATCAACACACAAATTTATGATCAAGTGAAGAAGTCTCTGGGCCAA	536
QY	977	GCAGTCTGTGGCTTTGATGTCTATCATACCATCAACATGTTCAAAAGCTGAAGTTGA	1036
Db	537	GCAGTCTGTGGCTTTGATGTCTATCATACCATCAACATGTTCAAAAGCTGAAGTTGA	596
QY	1037	CAAGTTTAAAGCAGCACATCCCTCTGGTGCAGAACTTGGCATCGATGACATTCATTT	1096
Db	597	CAAGTTTAAAGCAGCACATCCCTCTGGTGCAGAACTTGGCATCGATGACATTCATTT	656
QY	1097	TGATGACTTTTCTCTCGAGCTTGATGCCATGATCACAGCTCTCTCCGGATGTTTCATGGA	1156
Db	657	TGATGACTTTTCTCTCGAGCTTGATGCCATGATCACAGCTCTCTCCGGATGTTTCATGGA	716
QY	1157	GCTGGGATGTTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC	1216
Db	717	GCTGGGATGTTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC	776
QY	1217	AGTGAGAAACTATCGATGGTCTATACCAACCTGGAGACATGCTTCAACGCTGTG	1276
Db	777	AGTGAGAAACTATCGATGGTCTATACCAACCTGGAGACATGCTTCAACGCTGTG	836
QY	1277	TCAGCTGATTTCCGGATGTTAAACACTGCTGGGTTTCAAGACATTTCTGACCGAGTGGA	1336
Db	837	TCAGCTGATTTCCGGATGTTAAACACTGCTGGGTTTCAAGACATTTCTGACCGAGTGGA	896
QY	1337	AATTTAGGGTGATTTGGGATGCTGTGATGACCTCGACACAGGGGAACCAACAA	1396
Db	897	AATTTAGGGTGATTTGGGATGCTGTGATGACCTCGACACAGGGGAACCAACAA	956
QY	1397	TGCTTCCAGCTAGAGTGGCTGTGCTCCCTGGCCCACTCTATGGAACCTCTGCTACCTT	1456
Db	957	TGCTTCCAGCTAGAGTGGCTGTGCTCCCTGGCCCACTCTATGGAACCTCTGCTACCTT	1016
QY	1457	GGAGCATCACCATTTCACACCGCGGTGATGATCTCTCAAAAGTGGGCTCAACATATCTT	1516
Db	1017	GGAGCATCACCATTTCACACCGCGGTGATGATCTCTCAAAAGTGGGCTCAACATATCTT	1076
QY	1517	TGTAACCTGCTCCCAAGGAATATAGTGAACCTTATGACGCTTTTGAAGCAGTCAATAT	1576
Db	1077	TGTAACCTGCTCCCAAGGAATATAGTGAACCTTATGACGCTTTTGAAGCAGTCAATAT	1136
QY	1577	GGCAACACCTCAGCTGTACTTTGAGAGAGAGACTGAATTTCTTGAACCTTGCAGTAA	1636

Db	1137	GGCAACAGACCTCAGCGTGTACTTTTGAGAGAGAGAACTGAATCTTTGAACCTTGCAGTAA	1196
QY	1637	AGGAGATACGATTGGAAACATCAAAAACCATCGTGATATATTTTCGATCAATGTTAATGAC	1696
Db	1197	AGGAGATACGATTGGAAACATCAAAAACCATCGTGATATATTTTCGATCAATGTTAATGAC	1256
QY	1697	AGCCTGTGACCTTGGAGCCGTGACCAAAACCGTGGGAGATCTCCAGACAGTGGCAGAACT	1756
Db	1257	AGCCTGTGACCTTGGAGCCGTGACCAAAACCGTGGGAGATCTCCAGACAGTGGCAGAACT	1316
QY	1757	TGTAAACAGTCACTTCTCGAACAGAGAGATCGGGAGAGATTTAGAGCTCAAACTCACTCC	1816
Db	1317	TGTAAACAGTCACTTCTCGAACAGAGAGATCGGGAGAGATTTAGAGCTCAAACTCACTCC	1376
QY	1817	TTCAGCAATTTTGTATCGGAACCGGAGGATGAATGCTCGTGGTTCGAACCTGGAGTGGAT	1876
Db	1377	TTCAGCAATTTTGTATCGGAACCGGAGGATGAATGCTCGTGGTTCGAACCTGGAGTGGAT	1436
QY	1877	TGATAGCATCTGCATGCTTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAACCTGAAGCC	1936
Db	1437	TGATAGCATCTGCATGCTTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAACCTGAAGCC	1496
QY	1937	GATGCTAGATTCAGTAGCTACAAACAGAAAGTAAAGTGGGAGAGCTACACCAAAACGACT	1996
Db	1497	GATGCTAGATTCAGTAGCTACAAACAGAAAGTAAAGTGGGAGAGCTACACCAAAACGACT	1556
QY	1997	GCTGGCTCAACTGCTCCTCATCTCCCTGCGAGTGTATGTTAGTACCAAGGAGACAG	2056
Db	1557	GCTGGCTCAACTGCTCCTCATCTCCCTGCGAGTGTATGTTAGTACCAAGGAGACAG	1616
QY	2057	GAACATA 2063	
Db	1617	GAACATA 1623	
RESULT 8			
AAH78223			
ID	AAH78223	standard; DNA; 2513 BP.	
XX	AAH78223;		
AC	AAH78223;		
XX	26-NOV-2001	(first entry)	
DT	26-NOV-2001	(first entry)	
XX	Nucleotide sequence of a human phosphodiesterase polypeptide.		
DE	Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension;		
XX	nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism;		
KW	osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis;		
KW	Parkinson's disease; dementia; infectious disease; malignant tumour; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	1..1425	
FT	/*tag= a		
FT	/product= "phosphodiesterase"		
XX	WO200166716-A1.		
PN	13-SEP-2001.		
XX	06-MAR-2001; 2001WO-JP01720.		
XX	07-MAR-2000; 2000JP-0061464.		
PR	10-JUL-2000; 2000JP-0208610.		
XX	(KYOW) KYOWA HAKKO KOGYO KK.		
PA	Miyaaji H, Haruoka M, Ota T, Kawabata A, Sugano S, Nakamura Y;		
XX	WPI: 2001-570769/64.		
PI	P-PSDB; AAG67531.		
DR			
XX			

PT Polypeptides with phosphodiesterase activity and DNA for treatment of
PT diabetes, ischemic heart disease, hypertension, nephritis,
PT pancreatitis, ulcers, allergies, asthma
XX
PS Claim 3; Page 82-86; 105pp; Japanese.
XX

CC The present sequence encodes a human polypeptide which has
CC phosphodiesterase activity. The phosphodiesterase polypeptide and
CC polynucleotide are used for the treatment and prevention of diabetes,
CC ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers,
CC allergies, asthma, rheumatism, osteoporosis, pain, anxiety,
CC schizophrenia, manic depressive psychosis, Parkinson's disease,
CC dementia, infectious diseases, and malignant tumours.
XX

XX Sequence 2513 BP; 761 A; 528 C; 565 G; 659 T; 0 other;

Query Match	68.4%;	Score 1421.8;	DB 22;	Length 2513;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1423;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY 639	ATGGAGAATCATCATACTCCGACTGGCTAATAAATACAGCATTCGCTGAGCTGGTTCCT	698		
DB 1	ATGGAGAATCATCATACTCCGACTGGCTAATAAATACAGCATTCGCTGAGCTGGTTCCT	60		
QY 699	TCAACAGCCCTCCAGTGAACATCAGTATGCTTACCAGATCCGCGCTTTGATGCAGAG	758		
DB 61	TCAACAGCCCTCCAGTGAACATCAGTATGCTTACCAGATCCGCGCTTTGATGCAGAG	120		
QY 759	GCAGACCATATCTGTTTTCACATAAGATCTGTTCTTGTGTCCTTATTTGGAAATAGC	818		
DB 121	GCAGACCATATCTGTTTTCACATAAGATCTGTTCTTGTGTCCTTATTTGGAAATAGC	180		
QY 819	AACCACCAATTAATGGAGTGGCTCAAGCTTAAACAGACTTGTGGAAACCTTTTTCAT	878		
DB 181	AACCACCAATTAATGGAGTGGCTCAAGCTTAAACAGACTTGTGGAAACCTTTTTCAT	240		
QY 879	GATGCAGATCAACGACTTTTGGAGCTTTTGTATCTTTTGTGACTTTGGCATCAACAC	938		
DB 241	GATGCAGATCAACGACTTTTGGAGCTTTTGTATCTTTTGTGACTTTGGCATCAACAC	300		
QY 939	ACAATTATGATGATCAAGTGAAGAGTCCCTGGGCAAGCAGCTCTGTGGCTCTTTCATGTG	998		
DB 301	ACAATTATGATGATCAAGTGAAGAGTCCCTGGGCAAGCAGCTCTGTGGCTCTTTCATGTG	360		
QY 999	CTATCATACCATCAACATGTTTCAAAAGCTGAAGTTGACAAAGTTTAAAGCAGCCCAACATC	1058		
DB 361	CTATCATACCATCAACATGTTTCAAAAGCTGAAGTTGACAAAGTTTAAAGCAGCCCAACATC	420		
QY 1059	CCTCTGGTGTGAGAACTTGGCCATCGATGACATTCATTTTGTATGACTTTTCTCTCGACGTT	1118		
DB 421	CCTCTGGTGTGAGAACTTGGCCATCGATGACATTCATTTTGTATGACTTTTCTCTCGACGTT	480		
QY 1119	GATGCCATGATCAGACGCTCTCCGGATGTTTCATGGAGCTGGGATGGTACAGAAATTT	1178		
DB 481	GATGCCATGATCAGACGCTCTCCGGATGTTTCATGGAGCTGGGATGGTACAGAAATTT	540		
QY 1179	AAATATGACTATGAGACACTGTGTAGTGGCTTTTTCAGAGTGAAGAAACATATCGGATG	1238		
DB 541	AAATATGACTATGAGACACTGTGTAGTGGCTTTTTCAGAGTGAAGAAACATATCGGATG	600		
QY 1239	GTTCTATACCACTGGAGACATGCCCTTCAACGTGTGTACAGTGTATGTTCCGATGTTA	1298		
DB 601	GTTCTATACCACTGGAGACATGCCCTTCAACGTGTGTACAGTGTATGTTCCGATGTTA	660		
QY 1299	ACCACTGCTGGTTCACAGACATTCGACCGAGTGGAAATTTTAGCGGTGATTTGGGA	1358		
DB 661	ACCACTGCTGGTTCACAGACATTCGACCGAGTGGAAATTTTAGCGGTGATTTGGGA	720		
QY 1359	TGCCTGTGTGATGACCTGCACACAGGGGAACCAACATGCTTCCAAGCTAAGAGTGGC	1418		
DB 721	TGCCTGTGTGATGACCTGCACACAGGGGAACCAACATGCTTCCAAGCTAAGAGTGGC	780		
QY 1419	TCTGCCCTGGGCCAACTCTATGGAACCTCTGTACCTTTGGAGCATCACCATTTCACACC	1478		

DB 781	TCTGCCCTGGGCCAACTCTATGGAACCTCTGTACCTTTGGAGCATCACCATTTCACACC	840		
QY 1479	GCCGTGATGATCTTCAAGTGAGGTCACAAATATCTTTTGTCTTAACCTCTCTCCCAAGGAA	1538		
DB 841	GCCGTGATGATCTTCAAGTGAGGTCACAAATATCTTTTGTCTTAACCTCTCTCCCAAGGAA	900		
QY 1539	TATAGTAGACCTTATGACAGCTTTTGAAGCAGTCAATATTTGGCAACAGACCTCACGCTGTAC	1598		
DB 901	TATAGTAGACCTTATGACAGCTTTTGAAGCAGTCAATATTTGGCAACAGACCTCACGCTGTAC	960		
QY 1599	TTTGAGAGGAGAACTGAATCTTTTGAACCTTGTACGTAAGGAGATACGATTGGAAATC	1658		
DB 961	TTTGAGAGGAGAACTGAATCTTTTGAACCTTGTACGTAAGGAGATACGATTGGAAATC	1020		
QY 1659	AAAAACCATCTGATATATTTTCGATCAATGTTTAAATGACAGCTGTGACCTTTGGAGCCGTG	1718		
DB 1021	AAAAACCATCTGATATATTTTCGATCAATGTTTAAATGACAGCTGTGACCTTTGGAGCCGTG	1080		
QY 1719	ACCAAAACCTGGGAGATCTCCAGACAGGTGGCAGAACTTTGTAACCAAGTGAAGTTCTTCGAA	1778		
DB 1081	ACCAAAACCTGGGAGATCTCCAGACAGGTGGCAGAACTTTGTAACCAAGTGAAGTTCTTCGAA	1140		
QY 1779	CAAGGAGATCGGGAGAGATTAGAGCTCAAACTCACTCTTTCAGCAATTTTTCGATCGGAAC	1838		
DB 1141	CAAGGAGATCGGGAGAGATTAGAGCTCAAACTCACTCTTTCAGCAATTTTTCGATCGGAAC	1200		
QY 1839	CGGAAGGATGAACCTCCCTCGGTGGTCAACTGGAGTGAATTTGATAGCATCTGCAATGCTTTG	1898		
DB 1201	CGGAAGGATGAACCTCCCTCGGTGGTCAACTGGAGTGAATTTGATAGCATCTGCAATGCTTTG	1260		
QY 1899	TATCAGGACCTGGTGAAGTCAACGTGAAGCTGAAGCCGATGCTAGATTTCAGTAGTACA	1958		
DB 1261	TATCAGGACCTGGTGAAGTCAACGTGAAGCTGAAGCCGATGCTAGATTTCAGTAGTACA	1320		
QY 1959	AACGAAGTGAAGTGGGAAGAGCTACCAAAACGACCTGCTGGCTCAACTCCCTCATGCC	2018		
DB 1321	AACGAAGTGAAGTGGGAAGAGCTACCAAAACGACCTGCTGGCTCAACTCCCTCATGCC	1380		
QY 2019	TCCTCCCTCGGAGTGTATGATGACCAAGGAAGACAGAACTAA	2063		
DB 1381	TCCTCCCTCGGAGTGTATGATGACCAAGGAAGACAGAACTAA	1425		
RESULT 9	AAA49973			
ID	AAA49973	standard; cDNA; 1982 BP.		
XX	AAA49973;			
XX	AC			
DT	10-OCT-2000	(first entry)		
XX	Human cyclic nucleotide phosphodiesterase HSPDE10A2 cDNA.			
DE	Cyclic nucleotide phosphodiesterase; HSPDE10A2; human; cancer;			
KW	immune disorder; diagnosis; therapy; ss.			
XX	Homo sapiens.			
OS				
XX				
FT	Key	Location/Qualifiers		
FT	CDS	157..1260		
FT		/*tag= a		
XX				
PN	WO200040733-A1.			
XX				
PD	13-JUL-2000.			
XX				
PF	07-JAN-2000; 2000WO-US00371.			
XX				
PR	07-JAN-1999; 99US-0226741.			
XX				
PA	(INCY-) INCYTE PHARM INC.			
XX				

PI Phillips SC, Lanfear J, Fawcett L, Bandman O, Harrow I;
 XX WPI: 2000-452539/39.
 DR P-PSDB; AAY95522.
 XX
 PT New human cyclic nucleotide phosphodiesterases, referred as HSPDE10A1
 PT and HSPDE10A2, useful for treating and preventing cancer and immune
 PT disorders -
 XX
 XX
 PS Claim 4; Page 85-86; 96pp; English.
 XX
 CC The present sequence is that of cDNA encoding HSPDE10A2 (see
 CC AAY95522), a novel human cyclic nucleotide phosphodiesterase. The
 CC cDNA was initially identified in Incyte Clone 826776 from the
 CC prostate cDNA library PROSTUT04 using BLAST analysis and human
 CC phosphodiesterase 5 as query. Full-length cDNA sequences of
 CC HSPDE10A2 were obtained from a human skeletal muscle library using
 CC the complete cDNA insert of Incyte Clone 826776 as probe.
 CC HSPDE10A2 is a C-terminal splice variant of HSPDE10A1 (see AAY95521).
 CC The invention provides expression vectors, host cells, antibodies,
 CC agonists and antagonists, as well as methods for diagnosing,
 CC treating or preventing disorders associated with expression of
 CC HSPDE10A, especially cancer and immune disorders. A fragment of
 CC the present sequence from about nucleotide 1183 to nucleotide 1227
 CC is useful in hybridisation or amplification technologies to
 CC distinguish HSPDE10A2 sequences from related sequences.
 XX
 SQ Sequence 1982 BP; 592 A; 421 C; 425 G; 544 T; 0 other;

Query Match 50.3%; Score 1045.6; DB 21; Length 1982;
 Best Local Similarity 99.6%; Pred. No. 1.1e-314;
 Matches 1048; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 557 ACCAGTGTGAAATTTACCAATCTTTCAATTTGATGTCCTCCCAAGTCGATGCC 616
 DB 123 ACAGGTGGTGAATTTACCAATCTTTGAAATTTGATGTCCTCCCAAGTCGATGCC 182
 QY 617 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTAAATAATA 676
 DB 183 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTAAATAATA 242
 QY 677 GAGCATTCGTGAGCTGGTGTCTTCAACAGGCTTCCAGTGAACATCATGATGCCATCA 736
 DB 243 CAGCATTCGTGAGCTGGTGTCTTCAACAGGCTTCCAGTGAACATCATGATGCCATCA 302
 QY 737 GGATCCGCGCTTTGATGAGAGGAGAGCAGATATCTGTTTTCACATAAGATCTGTCT 796
 DB 303 GGATCCGCGCTTTGATGAGAGGAGAGCAGATATCTGTTTTCACATAAGATCTGTCT 362
 QY 797 TTGCTCCCTATTTGGAATAGCAACCAACCAATATTTGAGTGGCTCAAGTGTAAACAG 856
 DB 363 TTGCTCCCTATTTGGAATAGCAACCAACCAATATTTGAGTGGCTCAAGTGTAAACAG 422
 QY 857 ACTTGATGGGAACCTTTTGATGAGAGCAACCAAGCTTTTGGAGCTTTTGCATCTT 916
 DB 423 ACTTGATGGGAACCTTTTGATGAGAGCAACCAAGCTTTTGGAGCTTTTGCATCTT 482
 QY 917 TTGAGTCTTGCAATCAACACAAATATGATGATCAAGTGAAGAGCTCTGGGCAA 976
 DB 483 TTGAGTCTTGCAATCAACACAAATATGATGATCAAGTGAAGAGCTCTGGGCAA 542
 QY 977 GCAGTCTTGCTTGTATGCTATCATCATCAATGCAACATGTTCAAAAGCTGAAGTTGA 1036
 DB 543 GCAGTCTTGCTTGTATGCTATCATCATCAATGCAACATGTTCAAAAGCTGAAGTTGA 602
 QY 1037 CAAGTTTAAAGGAGCCACATCCCTCTGGTGTGAGAACTTGCATGATGATCATTT 1096
 DB 603 CAAGTTTAAAGGAGCCACATCCCTCTGGTGTGAGAACTTGCATGATGATCATTT 662
 QY 1097 TGATGACTTTTCTCGAGCTTGATGCGCATGATCACAGCTGCTCTCGGATGTCATGGA 1156
 DB 663 TGATGACTTTTCTCGAGCTTGATGCGCATGATCACAGCTGCTCTCGGATGTCATGGA 722

RESULT 10
 AAD28571
 ID AAD28571 standard; cDNA; 426 BP.
 XX
 AC AAD28571;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PDE-like enzyme encoding cDNA #2.
 XX
 KW Human; phosphodiesterase; PDE-like enzyme; benign prostate hyperplasia;
 KW urinary incontinence; erectile dysfunction; cardiovascular disorder;
 KW cancer; diabetes; ischaemic disease; myocardial infarction; cytostatic;
 KW vasodilator; cardiant; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..426
 FT /*tag= a
 FT /product= "Human PDE-like protein"
 FT /note= "CDS does not include start and stop codon"
 FT /partial
 XX
 PN WO200200854-A2.
 XX
 PD 03-JAN-2002.
 XX
 XX 26-JUN-2001; 2001WO-EP07289.
 XX
 XX 26-JUN-2000; 2000US-213998P.
 PR 25-MAY-2001; 2001US-293221P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Ramakrishnan S;
 XX
 DR WPI: 2002-090522/12.
 DR P-PSDB; AAD28571.
 XX

PT Isolated polynucleotide encoding a human phosphodiesterase-like enzyme,
PT useful for treating a disease such as urinary incontinence, benign
PT prostate hyperplasia, erectile dysfunction, diabetes, cancer or
PT cardiovascular disorder -

XX Claim 1b; Fig 4; 165pp; English.

XX The present invention relates to human phosphodiesterase (PDE)-like
CC enzymes and their corresponding polynucleotides. The invention also
CC relates to reagents which regulate PDE-like enzyme activity and reagents
CC which bind to human PDE-like enzyme gene products which can be used to
CC regulate degradation of cGMP. Sequences of the invention are useful for
CC modulating the activity of a PDE-like enzyme in a disease such as urinary
CC incontinence, benign prostate hyperplasia, erectile dysfunction, cancer,
CC diabetes or cardiovascular disorder (e.g. ischemic diseases, myocardial
CC infarction). The present sequence is a cDNA encoding human PDE-like
CC enzyme.

XX Sequence 426 BP; 137 A; 76 C; 94 G; 119 T; 0 other;

Query Match 18.7%; Score 388.8; DB 24; Length 426;
Best Local Similarity 99.5%; Pred. No. 2.3e-110;
Matches 390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 171 GATCGACGATCAATGATGAATCGACAAGCTGACTGATACAGACAAAATCAATTATG 230
DB 1 GATCGACGATCAATGATGAATCGACAAGCTGACTGATACAGACAAAATCAATTATG 60
QY 231 TGCATGCCATCCGAAGCAGTGATGCTGAGATTATTTGGTGGCCCAAGCGATATAAG 290
DB 61 TGCAATGCCATCCGAAGCAGTGATGCTGAGATTATTTGGTGGCCCAAGCGATATAAG 120
QY 291 ATTCTGTAAGGAGTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGATCTTCCA 350
DB 121 ATTCTGTAAGGAGTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGATCTTCCA 180
QY 351 TTTTGTGGAATCGGCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAGATATGAA 410
DB 181 TTTTGTGGAATCGGCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAGATATGAA 240
QY 411 AGAAGCAGAGCTTTGCTAGAGTGTTTAAATGACCTCTTTTGAAGACAGCTGACCTGGAG 470
DB 241 AGAAGCAGAGCTTTGCTAGAGTGTTTAAATGACCTCTTTTGAAGACAGCTGACCTGGAG 300
QY 471 AAAATTGTCAAGAAAATTAATGCATCGGGCCCAAACTCTGCTGAAATGTGAGCGTGTCT 530
DB 301 AAAATTGTCAAGAAAATTAATGCATCGGGCCCAAACTCTGCTGAAATGTGAGCGTGTCT 360
QY 531 GTTTTACTCTAGAGGACATCGAATCACCAGT 562
DB 361 GTTTTACTCTAGAGGACATCGAATCACCAGT 392

RESULT 11

AAA39042
ID AAA39042 standard; cDNA; 2499 BP.

XX AAA39042;

AC 25-AUG-2000 (first entry)

DE Human cGMP phosphodiesterase V encoding cDNA SEQ ID NO:2.

XX Human; cGMP phosphodiesterase V; inhibitor; tricyclic compound;
KW cyclic GMP phosphodiesterase inhibitor; erectile failure;
KW feminine function failure; ds.

XX Homo sapiens.

OS JP2000095759-A.

PN 04-APR-2000.

PD

XX

PF 19-JUL-1999; 99JP-0204103.

XX 21-JUL-1998; 98JP-0204963.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 2000-353412/31.

DR P-PSDB; AAY90912.

XX Tricyclic compounds having cyclic GMP-specific phosphodiesterase

PT inhibitory action useful as pharmaceuticals, and preparation and agents

PT thereof -

XX Example 117; Page 68-69; 71pp; Japanese.

PS The present invention describes cyclic GMP (cGMP)-specific

XX phosphodiesterase inhibitors comprising tricyclic compounds or their

CC salts. The inhibitors are useful for the treatment and prevention of

CC erectile failure and feminine function failure. The compounds have

CC excellent cGMP-phosphodiesterase inhibitory action. The present

CC sequence encodes human cGMP phosphodiesterase V, which is used in an

CC example from the present invention.

XX Sequence 2499 BP; 778 A; 493 C; 563 G; 565 T; 0 other;

QY Query Match 17.2%; Score 356.6; DB 21; Length 2499;

DB Best Local Similarity 52.0%; Pred. No. 7.7e-100;

QY Matches 954; Conservative 0; Mismatches 854; Indels 25; Gaps 6;

DB 159 AGGATCGAGCAATTCATGATGAATCGACACAGCTGACTGGATACAGACAAAATCATTTAT 228

DB 614 AGGATCTTCGTTCAATCGAAGTTGACCAAAATTCAGGCTACAGACAAAATCATTTAT 673

QY 229 TGTGATGCCATCCGAAGCAGTGATGCTGAGATTATTTGGTGGCCCAAGCGATAAATA 288

DB 674 TTTGATGCCAATTAAGAATCATAGGAAGAGTTGTTGGTGGCCCAAGCGCCATCAACA 733

QY 289 AGATTCTCTG---AAGGAGCTCCATTTACTGAAGATGATGAAAAGTTATGCAGATGATC 345

DB 734 AGAATCAGGAAACGCTGGACATTTACTGAAAAGATGAAAAGGACTTTGCTGCTTAT 793

QY 346 TTCCATTTTGGAAATCGGCATATCTAAGCTCAGCTCTTTGCTGCTCAAGGAAAGAT 405

DB 794 TGGCATTTTGGTATTTCTTCATAATGCTCAGCTCTATGAGACTTCTCAGCTGGAGA 853

QY 406 ATGAAGAACGACAGCTTTTGTAGAGTGGTTTAAATGACCTCTTTCAAGAACAGCTGACC 465

DB 854 ACAAGAGAAATCAGTGCTGCTTGACCTTGCTAGTTTAAATTTTGAAGAACAAATCAT 913

QY 466 TGGAGAAAATTTCAAGAAAATTAATGCTATCGGGCCCAAACTCTGCTGAAATGTGACGCT 525

DB 914 TAGAAGTAATTTTGAAGAAAATAGTCCACTATTATCTCTTTCATGCAAGTGCAGAAAT 973

QY 526 GTTCTGTTTTTACTCTAGAGGACATCGAATCACCAGTGGTGAATTTTACCAATCCTTTG 585

DB 974 GCACCAATTTTCATAGTGGATGAAGATTGCTCCGATTTCTTTTCTAGTGTGTTACATGG 1033

QY 586 AATTGATGTCCTCCCAAGTGCAGTGTGCTGAGAACAGTTTCAAGAACAGCTGGAGA 645

DB 1034 AGTGTGAGGAATTAGAAAATCATCTGATACATTAACAGGGAACATGATGCAACAAAA 1093

QY 646 AATCATCATCTCCGACTGGCTTAATAAATACAGCAATGCTGAGTGGTGTGCTTCAACAG 705

DB 1094 TCAATTACATGTATGCTCAGTATGCAAAAATACATGGAACCACTTAATATCCAGATG 1153

QY 706 GCTTCCAGTGAACATCAGT-----GATGCTCACCAGGATCCGCCCTTTGATGACAGGC 760

DB 1154 TCAGTAAGGATAAAAGATTTCCCTGGACAAATACAGAAAATGTAACACCAAGCAGT 1213

QY 761 AGACCAGATATCTGGTTTTTCATATAAGATCTGTTCTTTTGTGCTCCCTATTTTGAATAGCAA 820

DB 1214 GCATTAGAGTTTGTCTTTTGTACCTTATAAAAAATGGAAGAAAGAAATTAAGTTATAGGGG 1273

Qy	821	CCACCAATAATTGGAGTGGCTCAAGTGTAAACAGACTTGATGGGAAACCTTTTGATGA	880
Db	1274	TTTGCCAACTTGTTAATAAGATGGAGAGAAATATGCG--AAGGTTAAGCTTTTCAACCG	1331
Qy	881	TGCAGATCAACGAGCTTTTTCAGGCGTTTGTCACTCTTTTGGACTTGGCATCAACACAC	940
Db	1332	AAATGACGACAGTTCTCGAAGCTTTGTCACTCTTTTGGCTGGGGATCCAGAACAC	1391
Qy	941	AAATTATGATGATCAAGTGAAGAAGTCTCGGGCCAAAGCAGTCTGTGCTCTTGATGTGCT	1000
Db	1392	GCAGATGATGAGCACTGGAGAGAGCCATGGCCACGAANAAGTCACTTTGAGGTCT	1451
Qy	1001	ATCATACCATGCAACATGTTCAAAGCTGAAGTTGACAAGTTTAAAGCAGCCAAACATCCC	1060
Db	1452	GTCGTATATGCTTTCAGCAGCAGAGGAAGAAACAAGAGAGCTACAGTCGTTAGCGGCTG	1511
Qy	1061	TCGTGGTCTCA-----GNACTTGCCATCGATGACATTCATTTTGATGACTTTCTCT	1111
Db	1512	TGTGGTGCCATCTGCCAGACCCCTTAAAAATTACTGACTTTAGCTTCAGTCACATTTGAGCT	1571
Qy	1112	CGAGCTTGTATGCCATGATCACAGCTGCTCTCCGGATTTTCATGAGCTGGGATGGTACA	1171
Db	1572	GTCTGATCTGGAACACACACTGTCTACAAATTCGGATGTTTACTGACCTCAACCTTGTCA	1631
Qy	1172	GAAATTTAAATTGACTATGAGACACTGTGTAGGTGGCTTTTGACAGTGAAGGAAAACTA	1231
Db	1632	GAACTCCAGATGAACACTGAGGTCTTTCAGATGGATTTTAAAGTCTTAAAGAAGATTA	1691
Qy	1232	TCGGATG---GTTCTATACCACACTGGAGACATGCCCTTCAAGCTGTGTCTAGCTGATGTT	1288
Db	1692	TCGGAAGAAATGTTGGCTATCATAAATGGAGACATGCCCTTTAATACAGCTCAGTGCATGTT	1751
Qy	1289	CGCGATGTTAAACACTGCTGGGTTTCAAGACATTTCTGACCGAGGTGGAAATTTTAGCGGT	1348
Db	1752	TGCTGCTCTAAAGCAGGCAAAATTCAGAACAGCTGACTGACCTGGAGATACTTGGATT	1811
Qy	1349	GATTTGGGATGCGCTGTGTCATGACCTCGACCACAGGGGAACCAAAATGCCCTTCCAAGC	1408
Db	1812	GCTGATTTGCTGCACTAAGACCACGATTTGGATCACCGTGGTGAATAACTCTTACATACA	1871
Qy	1409	TAAAGTGGCTCTGCCCTGCCCCAACHCTATGNAACCTCTGCTACCTTGAGAGATCACCA	1468
Db	1872	GCGAAGTGAACATCCACTTCCCCAGCTTTTACTG---CCATTCAATCATGGAACACCATCA	1928
Qy	1469	TTTCAACACCGCGTGATGATCTTCAAAGTGAAGGTCACAATATCTTTCTCAACCTGTC	1528
Db	1929	TTTGGACAGTGGCTGATGATTTAATAGTCAGGCAATCAGATTCCTAGTGGCCCTCTC	1988
Qy	1529	CTCCAAGGAATATAGTGACCTTATGCAAGCTTTTGAAGCAGTCAATATGGCAACAGACCT	1588
Db	1989	CATTGGAAGATATAAGACCACGTTGAAATAATCAAGCAAGCTATTTTAGCTACAGACCT	2048
Qy	1589	CAGCTGTACTTTGAGAGGAGACTGAATTTCTTTGAACTTGTCAAGTAAAGGAGAAATACGA	1648
Db	2049	AGCACTGTACATTAAGAGGCGAGAGAAATTTTGAACCTTATAAGAAAAAATCAATTCAA	2108
Qy	1649	TTGGAACATCAAAAACCATCGTGATATATTTCGATCAATGTTAATGACACCTTGTACCT	1708
Db	2109	TTTGGAAAGATCTTCATCAAAAGGAGTTGTTTGGCAATGCTGATGACAGCTTTGTATCT	2168
Qy	1709	TGGAGCGCTGACCAACCCGTGGGAGATCTCCAGACAGTGGCAGAACTTTGAACCACTGA	1768
Db	2169	TTCTGCNAATTACAAACCTTGGCCATTTCAAACCGATAGCAGAACTTGTACCACTGA	2228
Qy	1769	GTTCTTCGAACAAGGAGATCGGGAGAGATTTAGAGCTCAAACTCACTCTTTCAGCAATTTT	1828
Db	2229	ATTTTTTGATCAAGGAGACAGAGAGAGAAAAAAGAACTCAACATAGAAGCCCACTGATTAAT	2288
Qy	1829	TGATCGGAACCGGAAGATGAATGCCCTCGGTTTGCAACTGAGGTGATTCATGATGATCTG	1888
Db	2289	GAAACGGGAGAGAAAAAATAAATCCCAAGTATGCAAGTTTGGGTTTCATAGATGCCATCTG	2348
Qy	1889	CATGCGCTTTGTATCAGCGACTGGTGAAGGTCAACGTGAAACTCAAGCCGATGCTAGATTC	1948

Db	2349	CTTCCAACTGTATGAGCCCTGACCCACGTTGTCAGAGGACTGTTCCCTTTGCTAGATGG	2408	
Qy	1949	AGTAGCTACAAACAGAAAGTAAGTGGGAAGAGCT	1981	
Db	2409	CTGCAGAAAGACACAGGCAGAAATYGGCAGGCCCT	2441	
RESULT 12				
ID	AAZ95234	standard; DNA; 2499 BP.		
XX	AC	AAZ95234;		
XX	AC	AAZ95234;		
DT	05-JUN-2000	(first entry)		
XX	Human phosphodiesterase V	nucleotide sequence #2.		
XX	Phosphodiesterase V; human; hypertension; pulmonary hypertension;			
KW	atherosclerosis, cerebral infarction; allergic rhinitis; kidney failure;			
KW	diabetic complication; glaucoma; ds.			
XX	Homo sapiens.			
OS	WO200005383-A1.			
PN	03-FEB-2000.			
PD	19-JUL-1999;	99WO-JP03865.		
XX	21-JUL-1998;	98JP-0204964.		
PR	16-APR-1999;	99JP-0108974.		
XX	(TAKE) TAKEDA CHEM IND. LTD.			
PA	Tarui N, Doi T, Nakahama K;			
XX	WPI; 2000-182705/16.			
PI	P-PSDB; RAY78940.			
DR	New phosphodiesterase V	useful for screening potential		
DR	phosphodiesterase inhibitors for treatment of hypertensive and allergic	diseases.		
PT	Claim 1; Page 81-85; 96pp; Japanese.			
PS	This sequence represents a human phosphodiesterase V	nucleotide sequence.		
CC	The phosphodiesterase V protein, its fragments and salts are useful in	the identification of phosphodiesterase V inhibitors for use in the		
CC	treatment of hypertension, pulmonary hypertension, atherosclerosis,	cerebral infarction, allergic rhinitis, kidney failure, diabetic		
CC	complications, and glaucoma.			
XX	Sequence 2499 BP; 778 A; 493 C; 563 G; 665 T; 0 other;			
SQ	Query Match	17.28;	Score 356.6;	DB 21; Length 2499;
	Best Local Similarity	52.08;	Pred. No. 7.7e-100;	
	Matches 954; Conservative	0;	Mismatches 854;	Indels 25; Gaps 6;
Qy	169	AGGATCCACGATTTCATGATGTAATCCACAAGCTGACTGGATACACAGACAAAATCATTTAT	228	
Db	614	AGGATCCCGTTCATGTCAGAGTTGACCAAAATACAGGCTACAGACACACAGCATTC	673	
Qy	229	TGTGATCGCTATCCGAAGCAGTGATGGTGAGATTATTGGTGTGGCCCAAGCGATAATA	288	
Db	674	TTTGTATGCCAAATTAAGAATCATAGGGAAGAGGTTGTTGGTGTAGCCAGGCCATCAACA	733	
Qy	289	AGATTCCTG---AAGGAGCTCCATTTACTGAAAGATGATGAAAAAGTTATGCAGATGATC	345	
Db	734	AGAAATCAGGAACGGTGGGACATTTACTGAAAAGATGAAAAGGACTTTGCTGCTTATTT	793	
Qy	346	TTCCATTTTGTGGAATGCCATATCTAAACGCTCAGCTCTTTTGTGCTCAAGCAAGAAT	405	

Db 794 TGGCATTTTGGGTATTTGTTCTTCAATATGCTAGCTCTATGAGACTTCACTGCTGGAGA 853
Qy 406 ATGAAGAAGACAGAGCTTTTGTAGAGGTGGTTAATGACCTCTTTGAAGAAGACAGACTGACC 465
Db 854 ACAAGAGAATACAGTGTCTGCTTACCTTGTAGTTTAAATTTTGAAGAACAACAATCAT 913
Qy 466 TGGAGAAAATTTGTCAGAAAATATATGATCGGGGCCCAAACTCTGCTGAAATGTCAGCGCT 525
Db 914 TAGAAGTAATTTTGAAGAAAATAGCTGCCACTATATATCTCTTTCATGCAAGTCAGAAAT 973
Qy 526 GTTCTGTTTACTCTAGAGGACATCGAATCACCAGTGGTGAATTTTACCAAAATCCTTTTG 585
Db 974 GCACCATTTTTCATAGTGGATGAAGATTGCTCCGATTTCTTTTCTAGTGTGTTTTCACATGG 1033
Qy 586 AATTGATGTCTCCCAAGTCAGTCTGCTGATGCTGAGAACAGTTTCAAGAAAAGCATGGAGA 645
Db 1034 AGTGTGAGGAATTAGAAAAATCATCTGATACATTAAACAAGGGAACATGATGCAACAAAA 1093
Qy 646 AATCATCATCTCCGACTGGCTAATAATACAGCATTTGCTGAGCTGGTTCCTTCAACAG 705
Db 1094 TCAATTACATGTATGCTCAGTATGTCAAAAATACTATGGAACCACTTAAATATCCAGATG 1153
Qy 706 GCCTTCCAGTCAACATCAGT-----GATGCCCTACCAGGATCCGCTTTGATGTCAGAGGC 760
Db 1154 TCAGTAGGATAAAGATTTCCTTGGCAACTGAAAATACAGAAATGTAACACGACGT 1213
Qy 761 AGACCAGATATCTGGTTTTCACATAAGATCTGTTTGTGTCTCCCTATTTTGGAAATAGCAA 820
Db 1214 GCATTAGAAGTTTCTTGTACACTATATAAAATGGAAGAAGAAATAAAGTTATAGGG 1273
Qy 821 CCACCAATAATTTGGAGTGGCTCAAGTGTAAACAGACTTGTATGGGAACCTTTTGATGA 880
Db 1274 TTTGCCAACTTGTAAATAAGATGGAGGAGAAATACTGGC--AAGGTTAAGCCTTTCAACCG 1331
Qy 881 TGCAGATCAACGACTTTTGGAGCTTTTGTGCATCTTTGTGAGCTTGGCATCAACACAC 940
Db 1332 AATGACGAACAGTTTCTGGAAGCTTTTGTGCATCTTTTGTGCTTGGGATCCAGAACAC 1391
Qy 941 AATTATGATGATCAAGTGAAGAGTCTCTGGGCCAAGCAGTCTGTGGCTCTTGATGTCT 1000
Db 1392 GCAGATGTATGAAGCAGTGGAGAGAGCCATGCCAAGCAATGTTCACATTGGAGTTCT 1451
Qy 1001 ATCATACCATGCACATGTTTCAAAAGCTGAAGTTGACAAAGTTTAAAGCAGCCACATCCC 1060
Db 1452 GTCGTATCATCTTCAGCAGCAGAGGAGAAACAAGAGAGCTACAGTCTGTAGCGGCTGC 1511
Qy 1061 TCTGGTGTC-----GAACCTTGCATCGATGACATTCATTTTGATGACTTTTCTCT 1111
Db 1512 TGTGGTGCATCTGCCAGACCCCTTAAATTTACTGACTTTTACGCTTACGTTGAGCT 1571
Qy 1112 CGAGCTTGTATGCCATGATACAGCTGCTCTCCGGATGTTTCAAGCTTGGGATGGGTACA 1171
Db 1572 GTCTGATCTGGAACAGCAGCTGTGTACAAATTCGGATGTTTACTGACCTCAACCTTGTGCA 1631
Qy 1172 GAAATTTAAATTTGACTATGACACACTGTGTAGTGGCTTTTGACAGTGAGGAAAACTA 1231
Db 1632 GAACCTTCAGATGAACATAGAGTTCTTTGAGATGGATTTTAAAGTGTAAAGAAATTA 1691
Qy 1232 TCGGATG---GTTCTATACCAACTGAGACATGCTTCAACGTTGTGTGAGCTGATGTT 1288
Db 1692 TCGAAGATGTTGCTCTATCATATTTGGAGACATGCTTTTAAACAGCTCAGTGCATGT 1751
Qy 1289 CGCGATGTTAACCACTGCTGGGTTTTCAGACATTTCTGACCGAGGTGGAAATTTTAGCGGT 1348
Db 1752 TGCTGCTCTAAAGCAGCAAAATTCAGAACAAAGCTGACTGAACCTGGAGATACITGCATT 1811
Qy 1349 CATTTGTGGATGCTCTGTCTATGACCTCGACCAAGGGGAACCAATGCTTCCAAAGC 1408
Db 1812 GCTGATTGCTGCACATAAGCCACAGATTTTGGATCACCGTGTGTGAATACTCTTACATACA 1871
Qy 1409 TAAGAGTGGCTCTGCCCTGGCCCCAAGCTCTATGGAACCTCTGCTACCTTGGAGCATCACA 1468
Db 1872 CGAAGTGAACATCCACTTGGCCAGCTTTTACTG---CCATTCAATCATGGAACACCATCA 1928

Qy 1469 TTTCAACACCACCCGTGATGATCCTTCAAAGTGAAGGTCACAATATCTTTTGTAACTGTC 1528
Db 1929 TTTTACCAGTGCCTGATGATTTCTAATAGTCCAGGCAATCAGATTCTCAGTGGCCTCTC 1988
Qy 1529 CTCCAAGGAATATAGTACCTTATGCACGCTTTTGAAGCAGTCAATATTTGGCAACAGACT 1588
Db 1989 CATTGAAGATATTAAGACCAGCTTGAANAATTAATCAAGCAAGCTATTTTAGCTACAGACT 2048
Qy 1589 CACGCTGTACTTTGAGAGGAGAACTGAATCTTTGAACCTTGTCAAGTAAAGGAGAAATACA 1648
Db 2049 AGCACTGTACATTAAGAGCGCAGGAGAAATTTTGAACCTTATAGAAAAAATCAATTCAA 2108
Qy 1649 TTGGAACATCAAAAACCATCTGTGATATATTTTCGATCAATGTATTAATGACAGCTGTGACT 1708
Db 2109 TTTGGAAGATCCTCATCAAAAGGAGTGTGTTTTTGGCAATGCTGTATGACAGCTTGTGATCT 2168
Qy 1709 TGGAGCCGTGACCAAAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTGTAAACAGTGA 1768
Db 2169 TTCTGCAATTTACAAAACCTGGCCTATTTCAACAAGGATAGCAGAACTTGTAGCAACTGA 2228
Qy 1769 GTTCTTCAACAAGGAGATCGGAGAGATTAGAGCTCAAACTCACTCTTCTCAGCAATTTT 1828
Db 2229 ATTTTGTGATCAAGGAGACAGAGAGAAAGAACTCAACATAGAACCCACTGATCTAAT 2288
Qy 1829 TGATCGGAACCGAAGGATGAACCTCCCTCGGTTCGCACTGGAGTGGATTTGATAGCATCTG 1888
Db 2289 GAACAGGAGAGAAACAAATCCCAAGTATGCAAGTTGGGTTTCATAGATGCCATCTG 2348
Qy 1889 CATGCCCTTTGATCAGGCACCTGGTGAAGTCAACGTGAACGTGAAGCGGATGCTAGATCTC 1948
Db 2349 CTTGCAACTGTATGAGGCCCTGACCCACGTGTCAAGAGGACTGTTTCCCTTTGCTAGATGG 2408
Qy 1949 AGTAGCTACAACAGCAAGTAAAGTGGGAAGACT 1981
Db 2409 CTGCAGAAAGACAGGCAAAATGCCAGGCCCT 2441

RESULT 13
AAF99963

ID AAF99963 standard; cDNA; 2499 BP.

XX AAF99963;

XX 16-JUL-2001 (first entry)

XX Human phosphodiesterase-V cDNA.

XX Human; phosphodiesterase-V; PDE-V; antianginal; cardiant; hypotensive;
KW antiarteriosclerotic; antiallergic; antiasthmatic; nephroretropic;
KW immunostimulant; ophthalmological; vasotropic; pyrimidine-5-carboxamide;
KW cGMP-specific PDE inhibitor; heart disorder; allergy; immunodeficiency;
XX eye disorder; fertility; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FH CDS 1..2499

FT /*tag= a

FT /partial

FT /note= "this sequence does not contain a stop codon"

FT /product= "PDE-V"

XX WO200127105-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-JP07048.

XX 12-OCT-1999; 99JP-0289868.

XX (TAKE) TAKEDA CHEM IND LTD.

XX

Db 1949 GCTGATGCTGCACTAAGCCACGATTGGATCAACCGTGGTGTGAATAAATCTTTACATACA 2008
QY 1409 TAAGAGTGGCTGCTCCCTGGCCCACTCTATGGAACTCTGCTACCTTTGGAGCATCACCA 1468
Db 2009 GCGAAGTGAACATCCACTTGGCCAGCTTACTG---CCATTCAATCATGGAACACCATCA 2065
QY 1469 TTTCACCAACGCGGTGATGATCTTCAAGTGAAGGTGACAAATATCTTTGTTAACTCTGTC 1528
Db 2066 TTTTGACCAAGTGCCTGATGATCTTAATAGTCCAGGCAATCAGATTCTCACTGCGCCTCTC 2125
QY 1529 CTCACGAATATAGTACCTTATGACCTTTTGAAGCAGTCAATATTTGGCAACAGACCT 1588
Db 2126 CATTTGAAGAATATAGACCACTGTTGAAATATCAAGCAAGCTATTTTAGCTACAGACCT 2185
QY 1589 CACGCTGTACTTTGAGAGGAGAACTGAATCTTTTGAACCTTGTCAAGGAGGAGATAGA 1648
Db 2186 AGCACTGTACATTAAGAGCGAGGAGAAATTTTGAACCTTATAGAAAAATCAATCA 2245
QY 1649 TTGGAACATCAAAACCACTGATATATTTTCGATCAATGTTAATGACAGCTGTGACCT 1708
Db 2246 TTTGGAAGATCCTCATCAAAAGGAGTGTCTTTTGGCAATGCTGATGACAGCTTGTGATCT 2305
QY 1709 TGGAGCCCTGACCAACCTGGAGATCTCCAGACAGTGGCAGAACTTTGAACCACTGA 1768
Db 2306 TTCTGCAATTAACAAACCTGGCCCTATTCAACACGGATGACAGAACTTTAGCAACTGA 2365
QY 1769 GTTCTTCGAACAGGAGATCGGAGAGATTAGAGCTCAAACTCACTCTCTTCAGCAATTT 1828
Db 2366 ATTTTTCATCAAGGAGACAGAGAGAAAGAACTCAACATAGAACCCATGATCTAAT 2425
QY 1829 TGATCGGAACCGGAAGGATGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1888
Db 2426 GAACAGGAGAGAGAAACAAATCCCAAGTATGCAAGTTGGGTTTCATAGATGCAATCTG 2485
QY 1889 CATGCTTTGTATCAGGCACTGGTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1948
Db 2486 CTTCGAAGTGTATGAGGCTGAGCCCTGAGCCAGTGTGAGAGGAGCTTTTCCCTTTTCTAGATGG 2545
QY 1949 AGTAGCTACAAACAGAAAGTAAAGTGGGAGAGCT 1981
Db 2546 CTGCAGAAAGAACAGGCAAGAAATGCGAGGCCCT 2578

RESULT 15
ID AAX99393 standard; cDNA; 2645 BP.
AC AAX99393;
XX
XX 09-NOV-1999 (first entry)
XX Human cGMP-binding, cGMP-specific phosphodiesterase (cGB-PDE) cDNA.
DE Cyclic guanosine monophosphate; cGMP; phosphodiesterase; cGB-PDE; enzyme;
KW antibody; Enzyme linked immunoabsorbant assay; ELISA; human; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 12..2639
FT /*tag= a
FT /product= "cGB-PDE"
XX
XX US955583-A.
XX
XX 21-SEP-1999.
XX
XX 05-JUN-1995; 95US-0463949.
XX
XX 27-MAY-1994; 94US-0250847.
XX 27-MAY-1993; 93US-0068051.
XX 05-JUN-1995; 95US-0463949.
XX

PA (ICOS-) ICOS CORP.
PA (UYVA-) UNIV VANDERBILT.
XX (UNIW) UNIV WASHINGTON.
PI Beavo JA, Corbin JD, Ferguson KM, Francis SH, Kadlecak A;
XX Loughney K, McAllister-lucas LM, Sonnenburg WK, Thomas MK;
DR WPI: 1999-539597/45.
XX P-PSDB: AAY14991.
PT Antibodies specific for cGMP-binding, cGMP-specific
PT phosphodiesterase useful for detecting and modulating the enzyme
XX
XX Example 6; Columns 49-56; 42pp; English.
XX The invention provides nucleotide sequences encoding bovine and human
CC cyclic guanosine monophosphate (cGMP)-binding, cGMP-specific
CC phosphodiesterase (designated cGB-PDE). The enzymes can be recombinantly
CC expressed by standard recombinant methodology. Antibodies specifically
CC immunoreactive with the cGB-PDE enzyme may be used to modulate the
CC activity of the cGB-PDE enzyme. Additionally, they may be used in assays
CC (e.g. Enzyme linked immunoabsorbant assays (ELISAs)) to detect the
CC presence of the enzyme in biological samples. The present sequence
XX represents a cDNA encoding the human cGB-PDE enzyme.
SQ Sequence 2645 BP; 813 A; 537 C; 609 G; 686 T; 0 other:
Query Match 17.2%; Score 356.6; DB 20; Length 2645;
Best Local Similarity 52.0%; Pred. No. 8e-100;
Matches 954; Conservative 0; Mismatches 854; Indels 25; Gaps 6;
QY 169 AGGATCGACGATTCATGATGAAATCGACACAGCTGACTGGATACAGACAAAATCATTTAT 228
Db 751 AGGATCTCGGTTCAATCCAGAGCTTGACCAATACAGGCTACAGACACAAAGCATTC 810
QY 229 TGTGCATGCCATCCGAGCAGTGTGATGATGATTTGGTGTGCGCCACAGCGATAAATA 288
Db 811 TTTGTATGCCAATTAAGAATCATAGGAAAGAGTTGTTGGTGTAGCCGAGCCATCAACA 870
QY 289 AGATTCTCTG---AAGGAGCTCCATTACTGAAGATGATGAAAAGTTATGAGATGTATC 345
Db 871 AGAATCAGGAACCGTGGGACATTTACTGAAAAGATGAAAAGGACTTTTCTGCTTTAT 930
QY 346 TTCCATTTTGTGAAATCGCCATATCTAACGCTCAGCTCTTTGCTGCTCAAGGAAAGAAAT 405
Db 931 TGGCATTTTGTGATTTGTTCTTCTTCAATATGCTCAGCTATGAGACTTCACTGCTGGAGA 990
QY 406 ATGAAAGAACGACAGCTTTGCTAGAGTGGTTAATGACCTCTTTTGAAGACAGACTGACC 465
Db 991 ACAAGAGAAATCAGGTGCTGCTTGACCTTGCTAGTTTAAATTTTCAAGACAAACAATCAT 1050
QY 466 TGGAGAAAATTTCAAGAAAATTAATGATCGGGCCCAACTCTGCTGAAATGTGAGCGCT 525
Db 1051 TAGAAGTAATTTTGAAGAAAATAGCTGCCACTATATCTCTTTTCATGCAAGTGCAGAAAT 1110
QY 526 GTTCTGTTTACTCTCTAGAGGACATCGAATCACCAGTGGTGAATAATTTACCAAAATCCTTTG 585
Db 1111 GCACCAATTTTCATAGTGGATGAGATTGCTCCGATTTCTTTTCTAGTGTGTTTCCACATGG 1170
QY 586 AATTGATGTCCTCCAAAGTGCAGTCTGATGCTGAGACAGTTTTCAAAGAAAGCATGGAGA 645
Db 1171 AGTGTAGGAATTAGAAAAATCATCTGATACATTAACAAGGGAAACATGATGCAACAAAA 1230
QY 646 AATCATCATACTCCGACTGGCTTAATAATAACACAGATTGCTGAGCTGTTGCTTCAACAG 705
Db 1231 TCATTTACATGTATGCTCAGTATGCAAAAATATCTATGGAACCACTTAATATCCCATG 1290
QY 706 GCCTTCCAGTGAACATCAGT-----GATGCTTACCAGGATCCGCGCTTTGATGACAGGC 760
Db 1291 TCAGTAAGGATAAAAGATTTCCCTGGACAACTGAAATACAGGAAATGTAACACCAAGCAT 1350
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Db 1411 TTTGCCAACTGTTAATAGATGGAGAGATACTTGGC--AAGTTAAGCCTTTCAACCG 1468
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Db 1469 AAATGACGAACAGATTCTTGGAGCTTTTGTATCTTTTGTGCTTTGGGATCCAGAACAC 1528
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Qy 1001 ATCATACCATGCAACATGTTCAAAAGCTCAAGTTGACAAGTTTAAAGGAGGCCAACATCCC 1060
Db 1589 GTCGTATCATGCTTCAGCAGCAGAGAGAAACAAGAGAGCTACAGTCGTTAGCGGCTGC 1648
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Qy 1529 CTCCAAGGAATATAGTGACCTTATGACGCTTTTGAAGCAGTCAATATTGGCAACAGACCT 1588
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Qy 1589 CAGCTGTACTTTGAGAGAGAACTGAATTCCTTTGAACCTTGTCAAGTAAAGGAGAAATACA 1648
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Qy 1889 CATGCTTTGTATCAGCACTGTTGAAGGTCAACGTGAACCTGAAGCCGATGCTAGATTC 1948
Db 2486 CTTGCAACTGTATGAGGCCCTCACCCACGTCAGAGGACTGTTTCCCTTTGCTAGATGG 2545
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Db 2546 CTGCAGAAAGAACAGGCAAGAAATGCGAGGCCCT 2578

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Job time : 508 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 16:28:05 ; Search time 105 Seconds
(without alignments)
6069.279 Million cell updates/sec

Title: US-09-663-542-2
Perfect score: 2078
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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1503.8	72.4	1784	4	US-09-595-514-2
3	1045.6	50.3	1982	3	US-09-226-741-4
4	1045.6	50.3	1982	4	US-09-595-514-4
5	356.6	17.2	2645	1	US-08-480-547A-22
6	356.6	17.2	2645	1	US-08-250-847B-22
7	356.6	17.2	2645	2	US-08-463-949A-22
8	356.6	17.2	2645	3	US-08-464-410A-22
9	356.6	17.2	2645	5	PCT-US94-06066-22
10	345.2	16.6	1982	1	US-08-480-547A-12
11	345.2	16.6	1982	1	US-08-250-847B-12
12	345.2	16.6	1982	2	US-08-463-949A-12
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26	216.6	10.4	3789	1	US-07-872-644-2
27	216.6	10.4	3789	1	US-08-297-494-2

ALIGNMENTS

RESULT 1

US-09-226-741-2
; Sequence 2, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1784
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: HSPDE10A1
US-09-226-741-2

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			Indels	0;
			Gaps	0;
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Db	117	ACAGTGTGAAATTTACCAATCCTTTGAATTCATGTCGCCCAAGTGCAGTGCATGATGC	176	
Oy	617	TGAGAACAGTTTCAAGAACAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA	676	
Db	177	TGAGAACAGTTTCAAGAACAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA	236	
Oy	677	CAGCATTCCTGAGCTGGTTGCTTCAACAGGCTTCCAGTGAACATCAGTATGCTTACCA	736	
Db	237	CAGCATTCCTGAGCTGGTTGCTTCAACAGGCTTCCAGTGAACATCAGTATGCTTACCA	296	
Oy	737	GGATCCGCGCTTTCATGACAGGAGCAGACCATATCTGGTTTTCACATAAGATCTGTCT	796	
Db	297	GGATCCGCGCTTTCATGACAGGAGCAGACCATATCTGGTTTTCACATAAGATCTGTCT	356	
Oy	797	TTGTGTCCTATTTGGAAATAGCAACCAATAATTTGAGTGGCTCAAGTGTAAACAG	856	
Db	357	TTGTGTCCTATTTGGAAATAGCAACCAATAATTTGAGTGGCTCAAGTGTAAACAG	416	
Oy	857	ACTTGATGGGAAACCTTTTGTATGATGACAGATCAACAGCTTTTGGAGCTTTTGTATCT	916	
Db	417	ACTTGATGGGAAACCTTTTGTATGATGACAGATCAACAGCTTTTGGAGCTTTTGTATCT	476	

Qy	917	TTGTGGACTTGGCAATCAACAACAATATATGTATGATCAAGTGAAGAAGTCTCTGGGCCAA	976
Db	477	TTGTGGACTTGGCAATCAACAACAATATATGTATGATCAAGTGAAGAAGTCTCTGGGCCAA	536
Qy	977	GCAGCTGTGGCTCTTGATGTGCTATCATACCATGCAACATGTTCAAAAGCTGAAGTTGA	1036
Db	537	GCAGCTGTGGCTCTTGATGTGCTATCATACCATGCAACATGTTCAAAAGCTGAAGTTGA	596
Qy	1037	CAAGTTTAAAGCAGCAACATCCCTCTGGTGTCTCAGAACTTGCATCGATGACATTCATTT	1096
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Qy	1097	TGATGACTTTTCTCTCGACGTTGATGCCATGATCACAAGCTGTCTCCGGATGTTCAFGGA	1156
Db	657	TGATGACTTTTCTCTCGACGTTGATGCCATGATCACAAGCTGTCTCCGGATGTTCAFGGA	716
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Qy	1217	AGTGAGAAAAAATATCGGATGTTCTATACCAACTGGAGACATGCCCTTCAACGTGTG	1276
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Db	837	TCAGCTGAŦGTTCCGATGTTAACCACTGCTGGGTTTCAAGACATTTCTGACCGAGGTGGA	896
Qy	1337	AATTTTAGCGGTGATCTGGGATGCCCTGCTCATGACCTCGACACAGGGGAACCAACAA	1396
Db	897	AATTTTAGCGGTGATCTGGGATGCCCTGCTCATGACCTCGACACAGGGGAACCAACAA	956
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Db	1257	AGCCTGTGACCTTGGAGCCGTGACCAACCGTGGGAGATCTCCAGACAGGTGGCAGAACT	1316
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Db	1377	TTCAGCAATTTTTCATCGGAACCGGAGGATGAACCTCCCTCGGTTCGAAGTGGAT	1436
Qy	1877	TGATAGCATCTGCATGCCCTTTGTATCAGGCACCTGGTCAAGGTCAACGTTGAAGCC	1936
Db	1437	TGATAGCATCTGCATGCCCTTTGTATCAGGCACCTGGTGAAGTCAACGTTGAAGCC	1496
Qy	1937	GATGCTAGATTTCAGTAGCTACAAACGAAGTAAGTGGGAGAGCTACACAAACGACT	1996
Db	1497	GATGCTAGATTTCAGTAGCTACAAACGAAGTAAGTGGGAGAGCTACACAAACGACT	1556

Qy	1997	CGTGGCGCTCAACTGCCTCATCTCTCCGCCCTGCGCAGHGTATGGTAGCCCAAGGAACACAG	20551
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Db	1617	GAACATA 1623	

RESULT 2	
US-09-595-514-2	
Sequence 2, Application US/09595514	
Patent NO. 6416991	
GENERAL INFORMATION:	
APPLICANT: Phillips, Stephen C.	
APPLICANT: Lanfear, Jerry	
APPLICANT: Fawcett, Lindsay	
APPLICANT: Bandman, Olga	
TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES	
FILE REFERENCE: PF-0623-1 CIP	
CURRENT APPLICATION NUMBER: US/09/595,514	
CURRENT FILING DATE: 2000-06-14	
PRIOR APPLICATION NUMBER: 09/226,741	
PRIOR FILING DATE: 1999-01-07	
NUMBER OF SEQ ID NOS: 7	
SOFTWARE: FastSeq for Windows Version 3.0	
SEQ ID NO 2	
LENGTH: 1784	
TYPE: DNA	
ORGANISM: HOMO SAPIENS	
OTHER INFORMATION: HSPDEL0A1	
US-09-595-514-2	

Query Match	72.4%	Score 1503.8	DB 4	Length 1784
Best Local Similarity	99.9%	Pred. No. 0		
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			Indels	0
			Gaps	0
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QY	617	TGAGAACAGTTTCAAAGAAGCATGGAGAATCATCATCTCCGACTGGCTTAATAATAA	676	
Db	177	TGAGAACAGTTTCAAAGAAGCATGGAGAATCATCATCTCCGACTGGCTTAATAATAA	236	
QY	677	CAGCATTTGCTGAGCTGGTTGCTTCAACAGGCTTCAGTGAAACATCAGTGATGCCCTACCA	736	
Db	237	CAGCATTTGCTGAGCTGGTTGCTTCAACAGGCTTCAGTGAAACATCAGTGATGCCCTACCA	296	
QY	737	GGATCCGCGCTTTGATGCAGAGGCACACAGATATCTGGTTTTTACATAGATCTCTTCT	796	
Db	297	GGATCCGCGCTTTGATGCAGAGGCACACAGATATCTGGTTTTTACATAGATCTCTTCT	356	
QY	797	TTCTGTGCCCTATTTGGAAATAGCAACCACCAATAATTTGGAGTGGCTCAAGTGTTAAACAG	856	
Db	357	TTCTGTGCCCTATTTGGAAATAGCAACCACCAATAATTTGGAGTGGCTCAAGTGTTAAACAG	416	
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Db	537	GCAGTCTGTGGCTTCTTGATGTGCTATCATACCATGCAACATGTTTCAAAAAGCTGAAGTTGA	596	
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Qy	1157	GCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC	1216
Db	717	GCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC	776
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Qy	1337	AATTTTAGCGGTGATTTGTGGGATGCCGTGTCTATGACCTCGACACAGGGGAACCAACAA	1396
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Db	1377	TTCAGCAATTTTGTATCGGAACCGGAAGGATGAATGCTCCCTCGGTTGCAACTGGAGTGGAT	1436
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Db	1437	TGATAGCATCTGCATGCCCTTTGTATCAGGCACCTGGTGAAGGTCAACGTGAAACTGAAGCC	1496
Qy	1937	GATGCTAGATTGATAGCTACAAACAGAAGTAAAGTGGAGAGCTACACCAAAACGACT	1996
Db	1497	GATGCTAGATTGATAGCTACAAACAGAAGTAAAGTGGAGAGCTACACCAAAACGACT	1556
Qy	1997	GCTGGCCTCAACTGCCCTATCTCTCCCTGCCAGTGTATGTCAGCCAAAGGAACAG	2056
Db	1557	GCTGGCCTCAACTGCCCTATCTCTCCCTGCCAGTGTATGTCAGCCAAAGGAACAG	1616
Qy	2057	GAACATAA 2063	
Db	1617	GAACATAA 1623	

```

: GENERAL INFORMATION:
: APPLICANT: Phillips, Stephen C.
: APPLICANT: Lanfear, Jerry
: APPLICANT: Lanfear, Lindsay
: APPLICANT: Fawcett, Lindsay
: APPLICANT: Bandman, Olga
: TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDESS
: FILE REFERENCE: PF-0623 US
: CURRENT APPLICATION NUMBER: US/09/226,741
: CURRENT FILING DATE: 1999-01-07
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 1982
: TYPE: DNA
: ORGANISM: HOMO SAPIENS
: FEATURE:
: OTHER INFORMATION: HSPDE10A2
: US-09-226-741-4

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Best Local Similarity		99.6%	-Pred. No. 0		
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		0			
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Db	123	ACAGGTGGTGAAATTTTACCAGAAATTCCTTTGAAATGATGTCCTCCCAAGATGCAGTGCTGATGC	182		
Qy	617	TGAGACAGTTTCAAAGAAAAGCATGGAGAAATCATCATCTCCGACATGGCTAATAAATAAA	676		
Db	183	TGAGAACAGTTTCAAAGAAAAGCATGGAGAAATCATCATCTCCGACATGGCTAATAAATAAA	242		
Qy	677	CAGCATTTGCTGAGCTGGTGTCTTCAACAGGCCTTCCAGTGAACATCAGTATGCCTACCA	736		
Db	243	CAGCATTTGCTGAGCTGGTGTCTTCAACAGGCCTTCCAGTGAACATCAGTATGCCTACCA	302		
Qy	737	GGATCCCGCCTTTGATCGACAGGCGACAGATATCTGTGTTTTCCACATAGATCTGTTC	796		
Db	303	GGATCCCGCCTTTGATCGACAGGCGACAGATATCTGTGTTTTCCACATAGATCTGTTC	362		
Qy	797	TTGTGTCCTCATTTTGGAAATAGCAACCAACAAATAAATTTGGAGTGCTCAAGTGTTTAAACAG	856		
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Qy	857	ACTTGATGGGAAACCTTTTGATGATGCAGATCAACGACTTTTGTGAGCCTTTTGTGCATCTT	916		
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Qy	1037	CAAGTTTTAAGCGAGCCCAACATCCCTCTGGTGTCTCAGAACTTGCCATCGATGACATTCATTT	1096		
Db	603	CAGTTTAAGCGAGCCCAACATCCCTCTGGTGTCTCAGAACTTGCCATCGATGACATTCATTT	662		
Qy	1097	TGATGACTTTTCTCTCGACGTTGATGCCATGATCACAGCTGCTCTCCGGATGTTTCATGGA	1156		
Db	663	TGATGACTTTTCTCTCGACGTTGATGCCATGATCACAGCTGCTCTCCGGATGTTTCATGGA	722		
Qy	1157	GCTGGGGATGGTACAGAAAATTTAAAATGTGACTATGACACACTGTGTAGGTGGCTTTTGAC	1216		
Db	723	GCTGGGGATGGTACAGAAAATTTAAAATGTGACTATGACACACTGTGTAGGTGGCTTTTGAC	782		
Qy	1217	AGTGAGGAAAAAATFATCGGATGGTTCATACCACAACTGGAGACATGCCTTCAACGCTGTG	1276		
Db	783	AGTGAGGAAAAAATFATCGGATGGTTCATACCACAACTGGAGACATGCCTTCAACGCTGTG	842		
Qy	1277	TCAGCTGATGTTCCGCTATGTTTAAACCCTGCTGGCTTTTCAAGACATTTCTGACCGAGGTGGA	1336		

Db 843 TCAGCTGATGTTCCGGATGTTAACACATGCTGGGTTTCAAGACATCTGACCGAGGTGGA 902
QY 1337 AATTTAGCGGTGATGTTGGATGCTGTGTCATGACCTCGACACAGGGGAACCAAA 1396
Db 903 AATTTAGCGGTGATGTTGGATGCTGTGTCATGACCTCGACACAGGGGAACCAAA 962
QY 1397 TGCCTTCAAGCTAAGATGCTGTGCGCTCGCCCAACTCTATGGAACCTCTGCTACCTT 1456
Db 963 TGCCTTCAAGCTAAGATGCTGTGCGCTCGCCCAACTCTATGGAACCTCTGCTACCTT 1022
QY 1457 GGAGCATCACCAATTTCAACAGCGCGTGATGATCCTTCAAGTGAGGCTCACAATATCTT 1516
Db 1023 GGAGCATCACCAATTTCAACAGCGCGTGATGATCCTTCAAGTGAGGCTCACAATATCTT 1082
QY 1517 TGCTAACCTTGCTCCTCAAGGAATATAGTACCTTATGACGCTTTTGAAGCAGTCAATATT 1576
Db 1083 TGCTAACCTTGCTCCTCAAGGAATATAGTACCTTATGACGCTTTTGAAGCAGTCAATATT 1142
QY 1577 GGCAACAGACCTCAGCTGTACTTTTGAGGGA 1608
Db 1143 GGCAACAGACCTCAGCTGTACTTTTGAGGGA 1174

RESULT 4

US-09-595-514-4
; Sequence 4, Application US/09595514
; Patent No. 6416991
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfeart, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PE-0623-1 CIP
; CURRENT APPLICATION NUMBER: US/09/595,514
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1982
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDE10A2
US-09-595-514-4

Query Match 50.3%; Score 1045.6; DB 4; Length 1982;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 557 ACCAGTGTGAAATTTACCAATCCTTTGAATGATGTCGCCAAAGTGCAGTGTGATGC 616
Db 123 ACAGTGTGAAATTTACCAATCCTTTGAATGATGTCGCCAAAGTGCAGTGTGATGC 182
QY 617 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTACCTCGAGTGGCTTAATAATAA 676
Db 183 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTACCTCGAGTGGCTTAATAATAA 242
QY 677 CAGCATTCCTGAGCTGGTGTGTTCAACAGGCGCTTCCAGTGAACATCAGTGTGCTACCA 736
Db 243 CAGCATTCCTGAGCTGGTGTGTTCAACAGGCGCTTCCAGTGAACATCAGTGTGCTACCA 302
QY 737 GGATCCGGCTTTTGATGAGAGGAGACACAGATATCTGGTTTCCACATAAGATCTGTCT 796
Db 303 GGATCCGGCTTTTGATGAGAGGAGACACAGATATCTGGTTTCCACATAAGATCTGTCT 362
QY 797 TTGTGTCCTATTTGGAAATAGCAACCAACCAAAATATTTGAGTGGCTCAAGTGTAAACAG 856
Db 363 TTGTGTCCTATTTGGAAATAGCAACCAACCAAAATATTTGAGTGGCTCAAGTGTAAACAG 422
QY 857 ACTGTGAGGAAACCTTTTGATGATGACATGACAGGACTTTTTCAGGCTTTTTCATCTT 916

Db 423 ACTGTAGGGAAACCTTTTGTATGATGACATCAACGACTTTTGTAGGCTTTTGTATCTT 482
QY 917 TTGTGAGCTTGGCATCAACACACAAATATATGATCATCAAGTGAAGAAGTCTCTGGCCAA 976
Db 483 TTGTGAGCTTGGCATCAACACACAAATATATGATCATCAAGTGAAGAAGTCTCTGGCCAA 542
QY 977 GCAGTCTGTGCTCTTGTATGCTATCATACCATGCAACATGTTTCAAAAGCTGAAGTTGA 1036
Db 543 GCAGTCTGTGCTCTTGTATGCTATCATACCATGCAACATGTTTCAAAAGCTGAAGTTGA 602
QY 1037 CAAGTTTAAAGCAGCCCAACATCCCTCTGGTCTGAGAACTTCCCATGATGACATTCATT 1096
Db 603 CAAGTTTAAAGCAGCCCAACATCCCTCTGGTCTGAGAACTTCCCATGATGACATTCATT 662
QY 1097 TGATGACTTTTCTCTCGACGTTTGTATGCTATGATGATGATGATGATGATGATGATGAT 1156
Db 663 TGATGACTTTTCTCTCGACGTTTGTATGCTATGATGATGATGATGATGATGATGATGAT 722
QY 1157 GCTGGGATGTCAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGTGAC 1216
Db 723 GCTGGGATGTCAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGTGAC 782
QY 1217 AGTGAGGAAACCTATCGGATGTTCTATACCAACCTGGAGACATGCTTCAACGCTGTG 1276
Db 783 AGTGAGGAAACCTATCGGATGTTCTATACCAACCTGGAGACATGCTTCAACGCTGTG 842
QY 1277 TCAGCTGATGTTGCGGATGTTAAACACTGCTGGGTTTCAAGACATTTCTGACCGAGGTGGA 1336
Db 843 TCAGCTGATGTTGCGGATGTTAAACACTGCTGGGTTTCAAGACATTTCTGACCGAGGTGGA 902
QY 1337 AATTTAGCGGTGATGTTGGATGCTGTGTCATGACCTCGACACAGGGGAACCAACAA 1396
Db 903 AATTTAGCGGTGATGTTGGATGCTGTGTCATGACCTCGACACAGGGGAACCAACAA 962
QY 1397 TGCCTTCCAACTAAGAGTGGCTCTGCGCTGGCCCAACTCTATGGAACCTCTGCTACCTT 1456
Db 963 TGCCTTCCAACTAAGAGTGGCTCTGCGCTGGCCCAACTCTATGGAACCTCTGCTACCTT 1022
QY 1457 GGAGCATCACCAATTTCAACAGCGCGTGATGATCCTTCAAAAGTGGGTCACAAATATCTT 1516
Db 1023 GGAGCATCACCAATTTCAACAGCGCGTGATGATCCTTCAAAAGTGGGTCACAAATATCTT 1082
QY 1517 TGCTAACCTGTCTTCCAAAGGAATATAGTACCTTTATGACGCTTTTGAAGCAGTCAATATT 1576
Db 1083 TGCTAACCTGTCTTCCAAAGGAATATAGTACCTTTATGACGCTTTTGAAGCAGTCAATATT 1142
QY 1577 GGCAACAGACCTCAGCTGTACTTTTGAGGGA 1608
Db 1143 GGCAACAGACCTCAGCTGTACTTTTGAGGGA 1174

RESULT 5

US-08-480-547A-22
; Sequence 22, Application US/08480547A
; Patent No. 5652131
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharon H.
; APPLICANT: Kadlec, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,547A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 565213land, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32791
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 2645 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 12..2636
US-08-480-547A-22

Query Match 17.2%; Score 356.6; DB 1; Length 2645;
Best Local Similarity 52.0%; Pred. No. 1.6e-105;
Matches 954; Conservative 0; Mismatches 854; Indels 25; Gaps 6;

QY 169 AGGATCGAGATTCATGATGAATCGACAAGCTGACTGGATACAGACAAAATCATAT 228
DB 751 AGGATCCTCGGTTCATGAGAGAGTTCACCAATTTACAGGCTACACAGACACAAGCATTC 810

QY 229 TGTGATCGCTATCCCAAGCAGTGATGGTGAGATTATTGGTGGGCCCAAGCGATAAATA 288
DB 811 TTGTATGCCAATTAGAAATCATAGGAAGAGGTGGTGTAGCCAGGCCATCAACA 870

QY 289 AGATTCCTG---AAGGAGTCCATTTACTGAAGATGATGAAAAGTTATGCAGATGATC 345
DB 871 AGAAATCAGAAACGGTGGGACATTTACTGAAAAGATGAAAAGGACTTTGCTGCTTATT 930

QY 346 TTCCATTTTGTGAATCGCCATATCTAACGCTCAGCTCTTTGCTGCTCAAGAAAGAT 405
DB 931 TGGCATTTTGTGGTATTGTTCTTCATAATGCTCAGCTATGAGACTTCACTGCTGGAGA 990

QY 406 ATGAAAAGACAGAGCTTTGTAGAGTGGTTAATGACCTCTTTTGAAGAACAGACTGACC 465
DB 991 ACNAGAGAAATCAGTGTGCTGTGACCTTGCTAGTTAATTTTGAAGAACACAATCAT 1050

QY 466 TGGAGAAAATTGCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGACGCT 525
DB 1051 TAGAAGTAATTTTGAAGAAAATAGCTGCCACTATTATCTCTTTTCATGCAAGTCAAAAT 1110

QY 526 GTTCTCTTTTACTCCTTAGAGGACATCGAATCACCAGTGGTGAATTTACCAATCTTTG 595
DB 1111 GCACCAATTTTCAATGAGTGGATGAAGATTGCTCCGATCTTTTCTAGTGTGTTTCATG 1170

QY 586 AATTGATGTCCCAAGTGCAGTGTGATGCTGAGAACAGTTTCAAGAAAGCATGGAGA 645
DB 1171 AGTGTGAGNAATTAGAAAATCATCTGATACATTAACAGGGAACATGATGCAACAAAA 1230

QY 646 AATCATCATCTCCGACTGGCTAATAAATAACAGCATTTGCTGAGCTGGTGTCTTCAACAG 705
DB 1231 TCAATTACATGTATGCTCAGTATGTCAAAAATACTATGGAACCACTTAATATCCAGATG 1290

QY 706 GCCTTCCAGTGAACATCAGT-----GATGCCCTACCAGGATCCCGCTTTGTATCGAGGC 760

DB 1291 TCAGTAAGGATAAAGATTTCCCTGGACAACACTGAAATAACAGGAAATGTAAACCCAGCAGT 1350

QY 761 AGACCAGATATCTGGTTTTCACATAAGACTCTGTTCTTGTGTCCCTATTATTGGAAATAGCAA 820

DB 1351 GCATTAGAAGTTTGGCTTTGTACACCTTATAAAATGGAAGAAGATAAAGTTATAGGGG 1410

QY 821 CCACCAAAATAATTGGAGTGGCTCAAGTGTAAACAGACTTGTATGGGAAACCTTTTGTATGA 880

DB 1411 TTGGCCAACCTTGTTAATAAGATGGAGAGAATACTGGC--AAGGTTAAGCCTTTCAACCG 1468

QY 881 TGCAGATCAACGACTTTTGGAGCTTTTGTCACTTTTGGGACTTTGGGATCAACACAC 940

DB 1469 AATGACGAACAGATTCTTGGAGCTTTTGTCACTTTTGGGCTTTGGGATCAGACAC 1528

QY 941 AATTATGTATCAAGTGAAGAAAGTCTGGGCCAAGCAGTCTGTGGCTCTTTCATGTGCT 1000

DB 1529 GCAGATGTATGAAGCAGTGGAGAGCCATGGCCAAGCAANTGTCACATTTGAGGTTCT 1588

QY 1001 ATCATACCATGCAACATGTTCAAAAGCTGAAGTTGACAAAGTTTAAAGCGACCCAAACATCC 1060

DB 1589 GTCGTATCATGCTTCAGCAGCAGAGGAAGAAACAGAGAGCTACAGTCGTTAGCGCTGC 1648

QY 1061 TCTGGTGTC-----GAACTTCCCATCGATGACATTTCAATTTTTCATCATTCTCT 1111

DB 1649 TGTGGTGGCATCTGCCAGACCCCTTAAATTTACTGACTTTAGCTTCAGTGACTTTGAGCT 1708

QY 1112 CGAGCTTGATGCCATGATCACAGCTGCTCTCCGGATGTTTCATGAGCTGGGATGGTACA 1171

DB 1709 GTCTGATCTGGAACACAGCAGCTGTGTACAATTCGGATGTTTACTGACCTCACCCTTTGTGCA 1768

QY 1172 GAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGACAGTAGGAAAAACTA 1231

DB 1769 GAACTTCCAGATGAAACATGAGGTTCTTTGACAGATGGATTTTAAGTGTTAAGAAGAATTA 1828

QY 1232 TCGGATG---GTTCTATACCAACACTGGAGACATGCTTCAACGCTGTGTCAGCTGATGTT 1288

DB 1829 TCGGAAGAATGTTCGCTATCATAAATTTGGAGACATGCTTTAATPACAGCTCAGTGCATGTT 1888

QY 1289 CGCGATGTTAAACACATGCTGGGTTTCAAGACATCTTGACCGAGGTGAAATTTAGCGGT 1348

DB 1889 TGCTGCTCTAAAGCAGGCAAAATTCAGAACAGCTGACTGACCTGGAGATACTTGCATT 1948

QY 1349 GATTGTGGAGTGGCTGTGTCATGACCTCGACACAGGGGAACCAACAATGCCCTTCCAAGC 1408

DB 1949 GCTGATTGCTGCACTAAGCCACGATTTGGATCACCCTGGTGTGAATAAATCTTACATACA 2008

QY 1409 TAAGAGTGGCTGCTGCCCTGCCCAACTCTATGAAACCTCTGCTACCTTGAGCATCACCA 1468

DB 2009 GCGAAGTGAACATCCCACTTGGCCAGCTTTACTG---CCATTTCAATCATGGAACACCATCA 2065

QY 1469 TTTCAACCCAGCGCTGATGATCCTTCAAGTGAAGGTGACAAATATCTTCTTAACCTGTC 1528

DB 2066 TTTTGACCAGTGCCTGATGATCTTAAATAGTCAGGCAATCAGATTTCTAGTGGCCTCTC 2125

QY 1529 CTCCAAGGAATAATGAGCTTATGACGCTTTTGAAGCAGTCAATATTTGCAACAGACACT 1588

DB 2126 CATTTGAAGAATAATAAGCACCGTTGAAAATAATAACAAGCAAGCTATTTTAGCTACAGACT 2185

QY 1589 CAGGCTGTACTTTGACAGGAGAACTGAATTTTGAACCTTGTCAGTAAAGGAGAAATACGA 1648

DB 2186 AGCACTGTACATTAAGGCGGAGAGAAATTTTGAACCTTATAGAAAATAATCAATTTCAA 2245

QY 1649 TTGGAACATCAAAAACCATCTGATATATTTTCGATCAATGTTAATGACACCTGTGACCT 1708

DB 2246 TTTGGAAGATCTTCATCAAAAGGAGTTGTTTTTGGCAATGCTGATGACAGCTTGTGATCT 2305

QY 1709 TGGAGCGTGACAAAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTTGTAACCACTGA 1768

DB 2306 TTCTGCAATTACAAAACCGTGGCTTATTCACAACGAGATAGCAAACTTGTAGCACTGA 2365

QY 1769 GTTCTTCGAACAGGAGATCGGGAGAGATTAGAGCTCAAACTCCTCCTTCACCAATTTT 1828

DB 2366 ATTTTGTGATCAAGGAGACAGAGAGAAAAGAACTCAACATAGAAACCCACTGATCTAAT 2425

Db 1231 TCAATTACATGATGCTCAGTAAGTCAAAAATACTATGGAACCACTTAATATCCAGATG 1290
Qy 706 GCCTTCCAGTGAACATCAGT-----GATGCTTACCAGATCGCGCTTTGATGAGAGGC 760
Db 1291 TCAGTAAGATAAAGATTTCCCTGGCACTGAAATACAGGAATGTAACACAGCAGT 1350
Qy 761 AGACAGATATCTGTTTTTCATATAAGATCTGTTCTTTGTGTCCTTATTTGGAATAGCAA 820
Db 1351 GCATTTAGAAGTTGCTTTGTACACCTATAAATAATGGAAGAGATAAAGTTATAGGGG 1410
Qy 821 CCACCAATAATTTGAGTGGCTCAAGTGTATAACAGACTTGATGGAAACCTTTTGATGA 880
Db 1411 TTTGGCAACTTGTTAATAAGATGGAGGAGATACTGGC--AAGGTTAAGCCCTTTCAACCG 1468
Qy 881 TGCAGATCAACGACTTTTGGAGCTTTTGTCTATCTTTTGTGCTGCTGTCATCAACAAC 940
Db 1469 AATGACGACAGTTTCTGGAAGCTTTTGTCTATCTTTTGTGCTGCTGTCATCAACAAC 1528
Qy 941 AATTATGATGATCAAGTGAAGTCTCTGGCCCAAGCAGTCTGTGGCTCTTTGATGTGCT 1000
Db 1529 CGAGATGATGAGCAGTGGAGAGCCATGGCCCAAGCAATGTCACATTTGGAGTTCT 1588
Qy 1001 ATCATACATGACATGTTTCAAAAGCTGAAGTTGACAAGTTTAAGGAGGCAACATCCC 1060
Db 1589 GTCGTATCATGCTTCAGCAGCAGAGAGAAACAAGAGAGCTACAGTCTGTAGCGGCTGC 1648
Qy 1061 TCTGTGTCA-----GAACCTGGCCATCGATGACATTCATTTTGTGATGACTTTCTCT 1111
Db 1649 TGTGTGGCTCTGCCAGACCTTTAAATTAATGATGCTTGTGCTTGTGATGACTTTGAGCT 1708
Qy 1112 CGACCTTGATGCCATGATCACAGTGTCTCCGGATGTTTCATGGAGCTGGGGATGGTACA 1171
Db 1709 GTCATGCTGAAACAGCAGCTGTGTACAAATTCGGATGTTTACTGACCTCAACCTTGCA 1768
Qy 1172 GAAATTTAAATTTGACTATGACACTGTGTAGTGGCTTTTGACAGTGAAGAAACTA 1231
Db 1769 GAACCTTCAGATGAACATAGGTTCTTTGAGATGGATTTTAAGTGTAAAGAGAATA 1828
Qy 1232 TCGGATG---GTTCTATACCAACTGGAGACATGCTCCCTTCAACGTGTGTACAGTGTCT 1288
Db 1829 TCGGAGATGTTGCCATATATATTTGGAGACATGCTTTAATACAGCTCAGTGCATGTT 1888
Qy 1289 CGGAGTTTAACTGCTGTGGTTTCAAGACATTTCTACCGAGGTGGAAATTTTACGGGT 1348
Db 1889 TGCTGCTTAAAGCAGGCAAAATTCAGAAAGCTGACTCACCTGGAGATACCTTGCATT 1948
Qy 1349 GATTCTGGATGCTGTGTATGACCTCGACACAGGGAACCAACATGCTTCCAGC 1408
Db 1949 GCTGATTCGCTGACTAAGCCACGATTTGGATCACCCTGTTGTAATACTTTACATACA 2008
Qy 1409 TAAGATGGCTCTGCTGCTGCCCCAATCTATGGAACCTTCTGCTACCTTTGGAGCATCACA 1468
Db 2009 CGGAGTGAACATCCACTTGCACCTTACGTTTACG---CCATTCATCATGGAACACCATCA 2065
Qy 1469 TTTCAACACCGCTGATGATCTTTCAAGTGAAGGTGACAAATATCTTTGCTAACCCTGTC 1528
Db 2066 TTTTGACCACTGCTGATGATTTCTTAATAGTCCAGGCAATCAGATTTCTCAGTGGCTCTC 2125
Qy 1529 CTCCAAGAAATAGTGAACCTTTATGACCTTTTGAAGCAGTCAATATTTGGCAACAGCCT 1588
Db 2126 CATTAAGAAATATAGACCACTGTTGAAATAATCAAGCAAGCTATTTTAGCTACAGACCT 2185
Qy 1589 CACGCTGTACTTTGAGAGGAGAACTGAATTTCTTGAACCTTGTCACTAAGGAGATACGA 1648
Db 2186 AGCACTGTACATTAAGAGCGAGAGATTTTGTGAACCTTATAGAAAAATCAATCAAA 2245
Qy 1649 TTGGAACATCAAAACCATCTGTATATTTTCGATCAATGTATGACAGCCTGTGACCT 1708
Db 2246 TTTGGAAGATCTCTATCAAAAGAGTGTGTTTTTGGCAATGCTGATGACAGCTTGTGATCT 2305
Qy 1709 TGGAGCCGTGACCAACCGTGGAGATCTCCAGCAGGTGCGCAACTTGTAAACCATGA 1768

Db 2306 TTCTGCAATTAACAAAACCTGGCCTATTTCACACGAGATAGCAGAACTTTAGCAACTGA 2365
Qy 1769 GTTCTTCAACAAGCAGATCGGAGAGATTAGAGCTCAAACTCACTCTCTTTCAGCAATTTT 1828
Db 2366 ATTTTGTATCAAGGAGACAGAGAGAAAGAACTCAACATAGAACCCACTGATCTAAT 2425
Qy 1829 TCATCGGAACCGGAGGATGAATCGCTCGGTTTCAACTGGAGTGGATTGATAGCATCTG 1888
Db 2426 GAACAGGAGAGAAACAAATCCCAAGATGCAAGTTGGTTTCATAGATGCCATCTG 2485
Qy 1889 CATGCTTTTATCAGGCACCTGGTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1948
Db 2486 CTTCGAACCTGTATGAGCCCTGACCCACCTGTCAGAGGACTGTTTCCCTTTGCTAGATGG 2545
Qy 1949 AGTAGCTACAACACAGCTAAGTGGGAAGCT 1981
Db 2546 CTGCAGAAAGAACACAGGAGCAAAATGGCAGGCCCT 2578

RESULT 8

US-08-464-410A-22
; Sequence 22, Application US/08464410A
; Patent No. 6037119
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharon H.
; APPLICANT: Radlecek, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464.410A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037119and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2645 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 12..2636
US-08-464-410A-22

Query Match

17.2%; Score 356.6; DB 3; Length 2645;

Best Local Similarity		52.0%;	Pred. No. 1.6e-105;			Indels	25;	Gaps	6;
Matches		954;	Conservative	0;	Mismatches	854;			
QY	169	AGGATCGACGATTC	CAATGATGAAATCG	ACAAAGCTG	AGATGAAATCG	ACAAATCAATAT	228		
Db	751	AGGATCGGCTT	CAATGACAAAGT	TGACCAATTA	AGGCTACAAAGCA	CAAGCATTC	810		
QY	229	TGTCATGCTT	ATCGGAAGAGT	GATGATGAT	TGTTGGTGGCC	CAAGCAATATA	288		
Db	811	TTTGTATGCAAT	TAAGAATCAT	AGGAAGAGT	TGTTGGTGTAG	CCAGCCATCAACA	870		
QY	289	AGATTCG	---AGGACCT	CAATTA	CTAGTGAAT	GATGAAAGTAT	GCAGATGATC	345	
Db	871	AGAAATCAGGA	ACGGTGGGACAT	TTACTGAAAGAT	GAAAGACAT	TTGCTGCTTAT	930		
QY	346	TTCCATTTGGA	ATCCCATAT	CTAACGCT	ACAGCTTT	GCTGCCCTCAAGGAAGAT	405		
Db	931	TGGCATTTT	GGTATGTTCT	TCTATATG	CTCAGCTAT	GACATTCAC	TGCGGAGA	990	
QY	406	ATGAAGAAG	CAGAGCTTT	GTAGAGT	GGTTAAT	GACCTCTTT	GAAGAACAGCTGACC	465	
Db	991	ACAAGAGAA	ATCAGGTGCT	GTGACCT	TTGCTAGT	TTAATTTT	CAAGCAACAATCAT	1050	
QY	466	TGGAGAAAT	TGTCAGAAAT	ATATGCT	CGGGCCCAAC	TCTGCTGAAAT	TGTGAGCGCT	525	
Db	1051	TAGAAGTAA	TTTGAAGAAAT	ATAGCTGCC	ACTATAT	TCTTTCTATGCAAGT	TGCAGAAAT	1110	
QY	526	GTTCGTGTT	ACTCTAGAGGACAT	CGAATC	CACAGTGGT	GAAATTTACCAAAAT	CCTTTG	585	
Db	1111	GCACCATTT	TCATAGT	GTGATGCT	CGGATTTCT	TTTCTAGTGT	TTTTCACATGG	1170	
QY	586	AATTGATG	CCCCAAAGT	GCAGTGT	GTGAGAACAGT	TTTCAAGAAAGCAT	GGAGA	645	
Db	1171	AGTGTGAGGA	ATAGAAAAAT	CATGATACAT	TAAACAGGGA	ACATGATCAACA	AAAA	1230	
QY	646	AATCATAT	ACTCCGACT	GGCTTA	ATAATACAGCAT	TGCTGAGCT	TTGCTTCAACAG	705	
Db	1231	TCAATAT	AGATGCT	AGTATGCT	CAAAAAT	ACTATGGAACCACT	TTAATATCCAGATG	1290	
QY	706	GCCTTCCAGT	CAACATCAGT	-----	GATGCCAT	CACAGGATCGCGCT	TTTGTAGCAGAGGC	760	
Db	1291	TCAGTAAGGA	TAAAGATTT	CCCTGGCACT	GAATACAGGA	AAATGAACAGCAGT	1350		
QY	761	AGACAGAT	ATCTGGTTT	TCATAGAT	CTGTTCTTT	TGTGCTCCTAT	TTTGGAAATAGCAA	820	
Db	1351	GCATTAGAAGT	TTGCTTTGT	TACCTATA	AAAAATGGA	AGAAATAAAGT	TATAGGG	1410	
QY	821	CCACCAAT	ATTTGGAGT	GGCTCAAGT	TTAAACAGCT	TTGATGGAAACCT	TTTGTATGA	880	
Db	1411	TTTGCCACT	TTGTTAAT	AAAGATGG	AGGAGATACT	GGC--	AAGGTTAAGCCCTTTCAACCG	1468	
QY	881	TGCAGATCA	ACGACTTTT	TGAGGCTTT	TGTCATCTTT	TGAGCTTTG	GCATCAACAACAC	940	
Db	1469	AAATGACGA	ACAGTTC	GGAGCTTT	TGTCATCTTT	TGCTTTGCGCT	TGGGATCCAGAACAC	1528	
QY	941	AATTATGAT	GATCAAGT	GATGATGCT	CTGGCCCAAGCAGT	CTCTGGCTCT	TTGATGCT	1000	
Db	1529	GCAGATGAT	GAAGCAGT	GGAGAGCCT	AGCAATGCT	CAATTTGAGGTTCT	1588		
QY	1001	ATCATACCAT	GCACATCTT	CAAGCTG	AGTTGACAA	AGTTTAAAGCAGCAACATCC	1060		
Db	1589	GTCGATCAT	GCTTCAGCAGG	AGGAGAAACA	AGAGAGCTT	ACATGCTTTAGCGGCTGC	1648		
QY	1061	TCTGTGTCA	-----	GAACIT	TGCCATCGAT	GACATTCATTT	TGATGACTTTCTCT	1111	
Db	1649	TGTGTGCCAT	CTGCCAGACCTT	AAATTA	CTGACTTT	AGCTTACATGACTTTGAGCT	1708		
QY	1112	CGAGTTGAT	GCCATGAT	CACAGT	GTCTCCGAT	GTTCATGAGCT	GGGATGGTACA	1171	
Db	1709	GTCTGAT	CTGGAACAGC	ACTGTGTACA	ATTCGGAT	TTTACTGACCTCAACCTTGTGCA	1768		
QY	1172	GAATTTAAAT	TGACTATG	ACACTGT	TAGGTGGCTTT	TGACAGT	GTGAGAAAACTA	1231	

Db	1769	GAATTC	CAGATGAAACAT	GAGGTTCTTT	GCAGATGGATTT	TAACTGTTAAAGAAATTA	1828		
QY	1232	TCGGATG	---GTTCT	TATACCAAC	ACTGGAGACAT	GCCTTTCAACGTTGCT	CAGCTGATCTT	1288	
Db	1829	TCGGAAG	AAATGTTGCC	TATCAT	TAATTTGGAGACAT	GCCTTTAATACAGCT	CAGTGCATCTT	1888	
QY	1289	CGGATGTT	AACCACTGCT	GGGTTTCA	AGACATCTG	ACCGAGGTGG	AAAAATTTTAGCGGT	1348	
Db	1889	TGCTGCT	CTAAAGCAGG	CAAAATTC	AGAACAAGCT	GACTGACCT	GGAGTACTTTGCAT	1948	
QY	1349	GATTGTGG	ATGCTGTCAT	GACCTCG	ACACAGGGGA	ACCAACATGCTT	TCCCAAGC	1408	
Db	1949	GCTGATT	GCTGCAT	TAAGCCAGAT	TTGGATCCCGT	GTGTGAATACT	CTTTACATACA	2008	
QY	1409	TAAAGT	GGCTCTG	CCCTGGCCCA	ACTCTATGG	AACTCTGCTACCT	TTGGAGCATCACCA	1468	
Db	2009	CGAAGT	GAAATCCACT	TTGCCAGCT	TTTACTG	---CCATTC	CAATCATGGAACACCATCA	2065	
QY	1469	TTTCAAC	CACCGCTGAT	GTATCCCTTCA	AAAGTGAAGG	GTCAATATCTTT	GTGTAAGCTGTC	1528	
Db	2066	TTTGGAC	CAATGCTGAT	GTATCTTA	TAGTCCAGGCA	ATCAGATTC	TCAGTGGCCTCTC	2125	
QY	1529	CTCCAAG	CAATATAGT	GACCTTATG	CAGCTTTT	GAAGCAGTCA	ATATTGGCAACAGACT	1588	
Db	2126	CATTGA	AGATATTAAG	ACCAGCTTT	GAAATTAATCA	AGCAAGCTAT	TTTAGCTACAGACT	2185	
QY	1589	CACGCT	GTACTTTGAG	AGGAGAACT	GAATCTTT	GAACTTTG	TCAGTAAGGAGATACGA	1648	
Db	2186	AGCACT	GTACATTAAG	AGCGGAGGA	AAATTTT	TGAACTTAT	NAGAAAAATCAATCAA	2245	
QY	1649	TTGGAAC	ATCAAAACCAT	CGTGTATAT	TTTCGATCA	ATGTTAAT	TGACAGCTGTGACCT	1708	
Db	2246	TTTGAAG	ATCCTCAT	CAAAAAGG	AGTCTTTT	TGGCAATGCT	GTATGACAGCTTTGTGATCT	2305	
QY	1709	TGGACCC	GTGACCAAC	CGTGGGAGAT	CTCCAGACAGT	GGCAGACTTT	TAACCACTGA	1768	
Db	2306	TTCTGCA	ATTAACAA	CCCTGGCCCTAT	TCAACAGG	ATAGCAACT	TTGTAGCAACTGA	2365	
QY	1769	GTCTT	CGAACAAGG	AGATCGG	GAGATTAAGT	CTCAACTCACT	CTCTTCAGCAATTTT	1828	
Db	2366	ATTTT	TTTTCATCA	AGGAGACAGAG	AGAAAGAACT	CAACATAGAAC	CCCACTGATCTAAT	2425	
QY	1829	TGATCGG	AAACCGGAAG	GATGAAC	TGCTCGGTTG	CAACTGGAGT	GGATTTGATAGATCTG	1888	
Db	2426	GAACAGG	CAGAGAA	AAAAA	CAAAATCCCA	AGTATGCAAGT	TGGGTTTATAGATGCCATCTG	2485	
QY	1889	CATGCT	TTGTATCAGG	CACCTGGT	GAAGTCAAC	GTGAACCTG	AACTGAAGCCGATGATATC	1948	
Db	2486	CTTGCA	ACTGTATGAG	CCCTGAC	CCACGCTG	TCAGAGGACT	GTTCCTCTTCTAGATGG	2545	
QY	1949	AGTAGCT	CAACA	AGAACTAAGT	GGGAAGCT	1981			
Db	2546	CTGCAGA	AAAGACAG	CGCAAAAT	TGCAGG	CCCT	2578		

RESULT 9
PCT-US94-06066-22
; Sequence 22, Application PC/TUS9406066
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Washington
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

QY 1349 GATTGTGGGATCCCTGTGTGATGATCCGACCTGACACAGGGAACCAACATGCTTCCAAGC 1408
Db 1430 GCTGATGCTGCACTAAGCCAGATTTGGATCACCCTGGTGTGAATAACTCTTACATACA 1489
QY 1409 TAAGAGTGGCTGCTGCCCTGGCCCAACTCTATGGAACCTCTGTACTCTTGGAGCATCACA 1468
Db 1490 GCGAAGTGAACATCCACTTGGCCAGCTTTACTG---CCATTCAATCATGGAACACCATCA 1546
QY 1469 TTTCACACCGCGTGTGATGATCCCTTCAAGAGTGGGTGCATATATCTTTGCTAACTGTC 1528
Db 1547 TTTTGACCAAGTGCCTGATGATCTTTAATAGTCCAGGCAATCAGATTCAGTGGCCTCTC 1606
QY 1529 CTCCAAGGAATAGTACCTTATCAGCTTTTGAAGCAGTCAATATTGGCAACAGACT 1588
Db 1607 CATTGAAGATATAGACCACCTGTGAATAATCAAGCAAGCTATTTAGCTACAGACT 1666
QY 1589 CAGCTGTACTTTGAGAGAGAACTGAATCTTTGAACCTTGTCACTAAAGAGAAATACGA 1648
Db 1667 AGCACTGTACATTAAGAGCGGAGGAGAAATTTTGAACCTTATAAGAAAAAATCAATTCAA 1726
QY 1649 TTGGAACATCAAAACCCTGTGATATATTTCCGATCAATGTTAATGACAGCTGTGACT 1708
Db 1727 TTTGGAAGATCTCTATCAAAAGAGTGTGTTTGGCAATGCTGTATGACAGCTTGTGATCT 1786
QY 1709 TGGAGCCGTGACCAACCGTGGGAGATCTCCAGACAGCTGGCAGAACTTGTAAACCAGTGA 1768
Db 1787 TTTCTCAATTAACAAACCTTGGCTTTTCAACACGGATAGCAGAACTTGTAGCAACTGA 1846
QY 1769 GTTCTTGAACAGGAGATCGGGAGATGATGAGCTCAAACTCACTCTCTTCCAGCAATTTT 1828
Db 1847 ATTTTGTATCAAGGAGACAGAGAGAGAAAGAACTCAACATAGAACCCACTGATCTAAT 1906
QY 1829 TGATCGGAACCGAGGATGAACTCCCTCGGTTTGAACCTGGAGTGGATGATAGACTGTG 1888
Db 1907 GAACAGGAGGAGAGAAACAAATCCCAAGTATGCAAGTGGGTTTCATAGATGCCATCTG 1966
QY 1889 CATGCTTTGTATCAG 1904
Db 1967 CTTGCAACTGTATGAG 1982

RESULT 11

US-08-250-847B-12
; Sequence 12, Application US/08250847B
; Patent No. 5702936
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecek, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250.847B

FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,051
; FILING DATE: 27-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5702936and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-250-847B-12

Query Match 16.6%; Score 345.2; DB 1; Length 1982;

Best Local Similarity 52.3%; Pred. No. 6.8e-102;

Matches 918; Conservative 0; Mismatches 813; Indels 25; Gaps 6;

QY 169 AGGATCGACGATTCATGATGAAATCGACAAGCTCACTGGATACAGACAAATCATTTAT 228
Db 232 AGGATCCCTCGGTTCATGCAAGCTTGACCAAAATACAGGCTTACAGACACAAACATTC 291
QY 229 TGTGATGCCCTATCCGAAGCAGTGTGATGATGATGTTGTTGGTGGCCCAAGCGATAAATA 288
Db 292 TTTGTATGCCAATTAAGAAATCATAGGGAAGAGTTGTTGGTGTAGCCAGGCCATCAACA 351
QY 289 AGATTCCTG---AAGGAGCTCCATTTACTGAAGATGATCAAAAAGTTATGACAGATGATC 345
Db 352 AGAAATCAGGAAACCGTGGACATTTACTGAAAAAGATGAAAAGACATTTGCTGCTTATT 411
QY 346 TTCCATTTTGTGAATGCCATATCTAAGCTCAGCTCTTTGCTGCTTCAAGGAAGAAT 405
Db 412 TGGCATTTTGTGTTATTTCTTCATAATGCTCAGCTCTATGAGACTTTCACCTGCTGGAGA 471
QY 406 ATGAAAGACGACAGCTTTGCTAGAGTGGTTAATGACCTCTTTTGAAGAACAGACTGACC 465
Db 472 ACAAGAGAAATCAGTGTGCTGCTTACCTGCTAGTTTAAATTTTGAAGAACACAAATCAT 531
QY 466 TGGAGAAATTTGTCAAGAAATAATGCTATCGGGCCCAAACTCTGCTGATAATGTGAGCGCT 525
Db 532 TAGAAGTAATTTTGAAGAAATAAGTGCACACTTATTATCTCTTTCATGCAAGTGCAGAAAT 591
QY 526 GTTCTGTTTACTCTCTAGAGCAGATCGAATCACCAGTGGTGAATTTTACCAATCCTTTG 585
Db 592 GCACCATTTTCATAGTGGATGAAGATTCCTCCGATTTCTTTCTAGTGTGTTTACATGG 651
QY 586 AATTGATGTCTCCCAAGTGCAGTGTGATGCTGAGAACAGCTTTCAAGAAAGCATGGAGA 645
Db 652 AGTGTGAGGAATAGAAAAATCATCTGATCATTAACAAGGGAACATCATGCAACAAAA 711
QY 646 AATCATCATCTCCGACTGGCTTAATAACAGCAATTTGCTGAGCTGTTGCTTCAACAG 705
Db 712 TCAATTACATGTATGCTCAGTATGTCAAAAATACTATGGAACCACTTAATATCCAGATG 771
QY 706 GCCTTCCAGTGAACA-----TCAGTGTGCTTACCAGATCCGCGCTTTGATGACAGAGC 760
Db 772 TCAGTAAGGATAAAGATTTCCCTGGACAATGAAATACAGGAATTAACCAAGCAGT 831
QY 761 AGACGAGATCTGTTTTCACATAAGATCTGTTCTTTGTTGCTCCCTATTTCGAATAGCAA 820
Db 832 GCATTAGAAGTTGCTTTGTACACCTATAAAAAATGGAAGAACAAATTAAGTTATAGGG 891
QY 821 CCACCAATAATTTGAGTGGCTCAAGTGTAAACAGACTTGAATGGGAACCTTTTGTATGA 880
Db 892 TTTGCCAACTTTGTTAATAAGATGGAGGAGATACTGCG---AAGGTTAAGCCTTTCAACCG 949

Qy 881 TGAGATCAACAGCAGCTTTTGGAGCTTTTGTGATCTTTTGGAGCTTGGCATCAACACAC 940
Dy 950 AAATGACGAACAGTCTTCTGGAAGCTTTTGTGATCTTTTGGAGCTTGGGATCCAGAACAC 1009
Qy 941 AATTATGATGATCAAGTGAAGAGTCTTGGGCAACAGCAGTCTGTGCTCTTGTATGCT 1000
Dy 1010 GCAGATGATGAAGCAGTGGAGAGCCATGGCCAAAGCAATGGTCAATGGAGGTTCT 1069
Qy 1001 ATCATACCATGCAACATGTTCAAAAGCTGAAGTTGACAAGTTTAAAGCAGCAACATCCC 1060
Dy 1070 GTCTATATGCTTCAGCAGCAGGAGGAAGAACAGAGAGCTACAGTCTGTAGCGGCTGC 1129
Qy 1061 TCRGGTGTGAG-----AACTTGGCATCGATGACATCATTTTGTATGATCTTTTCTCT 1111
Dy 1130 TGTGGTCCCATCTGCCACAGCCCTTAAATTTACTGACTTTTAGCTTTCAGTCACTTTGAGCT 1189
Qy 1112 CGAGTTGATGCCATGATCAGACGTCTCTCCGGATGTTTATGAGCTGGGATGGTACA 1171
Dy 1190 GTCTGATCTGGAACAGCAGCTGTGTACAATTCGGATGTTTACTGACCTCAACCTTGTGCA 1249
Qy 1172 GAAATTTAAATGACTATGAGACACGTGTGTAGTGGCTTTTGGACGTGAGGAAAACTA 1231
Dy 1250 GAACCTCCAGATGAACATCAGGTTCTTTCAGATGGATTTTAAAGTGTAAAGAAATTA 1309
Qy 1232 TCGGATG---GTTCTATPACCAACTGGAGACATGCTTCAACGTGTGTGAGCTGTATGTT 1288
Dy 1310 TCGGAAGAATGTTGCCATATCAATTTGGAGACATGCTTAAATACAGCTCAGTGCATGTT 1369
Qy 1289 CGGATGTTAAACCACTCTGGTTCGAAGACATCTGACCGAGGTGGAATTTTAGCGGT 1348
Dy 1370 TGTGCTTAAAGCAGCGCAAAATTCAGAACAGTCTGACTGACCTGGAGATCTTGCATT 1429
Qy 1349 GATTGTGGATGCTGTGTGATGACCTGACACAGCGGAGCAACAACTGCTTCCAGC 1408
Dy 1430 GCTGATTTGCTGCACTAGCAGCAGTTTGGATCACCGTGGTGTGAATCACTTTACATACA 1489
Qy 1409 TAAGAGTGGCTCTGCCCTGCCCACTCTATGGAACCTCTGCTACCTTGGAGCATCACCA 1468
Dy 1490 CGGAAGTGAACATCCACTTCCCAAGCTTTACTG---CCATTCATCATGGAACACCATCA 1546
Qy 1469 TTTCAACCAAGCGGTGATGATCTTCAAGTGAAGGTGCAATATCTTTGCTAACCTGTC 1528
Dy 1547 TTTTGACCACTGGCTGATGATCTTAAATAGTCCAGGCAATCAGATCTCAGTGGCTCTC 1606
Qy 1529 CTCAAGGAATATAGTGACCTTATGACGCTTTTGAAGCAGTCAATATTTGGCAACAGACT 1588
Dy 1607 CATTGAAGATATAGACAGCTTGAANAATCAACAGCAAGCTATTTTAGCTACAGACT 1656
Qy 1589 CAGCTGCTACTTTGAGAGGAGAACTGAATTTCTTTGAACCTTTGCTAGTAAAGGAGAAATCA 1648
Dy 1667 AGCACTGTACATTAAGAGCGAGGAGAAATTTTGAACCTTATAGAAAAAATCAATTCAA 1726
Qy 1649 TTGGAACATCAAAACCATCTGTGATATATTTTCGATCAATGTTAATGACAGCTGTGACCT 1708
Dy 1727 TTTGGAAGATCTCTCATCAAAAGAGTGTGTTTGGCAATGCTGTATGACAGCTTGTGATCT 1786
Qy 1709 TGGAGCGGTGACCAAAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTGTAAACAGTGA 1768
Dy 1787 TTCTGCAATTAACAACCCCTGGCCCTATTCACACAGGATAGCAGAACTTGTAGCAACTGA 1846
Qy 1769 GTTCTTCCAAAGAGATCGGAGATTAAGAGCTCAAACTCACTCTTCCAGCAATTTT 1828
Dy 1847 ATTTTGTGATCAAGGAGAGAGAGAGAAAGAACTCAACATAGAACCCACTGATCTANT 1906
Qy 1829 TGATCGAACCGGAGAGTGAACCTCGGTTCCACTCGGAGTGGATTTGATAGCATCTG 1888
Dy 1907 GAACAGGAG 1966
Qy 1889 CATGCCCTTGTATCAG 1904
Dy 1967 CTTCGAAGTGTATGAG 1982

RESULT 12
US-08-463-949A-12
Sequence 12, Application US/08463949A
Patent No. 5955583
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Corbin, Jackie D.
APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharon H.
APPLICANT: Kadlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5955583and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-463-949A-12

Query Match 16.6%; Score 345.2; DB 2; Length 1982;
Best Local Similarity 52.3%; Pred. No. 6.8e-102;
Matches 918; Conservative 0; Mismatches 813; Indels 25; Gaps 6;
Qy 169 AGGATCAGCAGTTCATCAATGATGAAATCGACAGCTGACTGGATACAGACAAATCATTTAT 228
Dy 232 AGGATCCTCGGTTCAATGACAGAGTTGACCAAAATACAGGCTACAGGACACAAAGCATTC 291
Qy 229 TGTCATGCTCTATCCGAGCAGTGTGATGAGATTTATTGGTGTGCGCCCAAGCAGATAAATA 288
Dy 292 TTTGATGCCAATTAAGAATCATAGGAAGAGGTTGTGGTGTAGCCCGCCATCAACA 351
Qy 289 AGATTCCTG---AAGGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATC 345
Dy 352 AGAATCAGGAACCGTGGGACATTTACTGAAAAAGATGAAAGAGACTTTGCTGCTTATT 411
Qy 346 TTCCATTTTGGGAATGCCCATATCTAACGCTCAGCTCTTTGCTGCTCAGGAAAGANT 405
Dy 412 TGGCATTTTGTGGTATTGTTCTTCATATGCTCAGCTCTATGAGACTTTCAGTGTGAGA 471

QY 406 ATGAAGAAGCAGAGCTTTTGTAGAGTGGTTAATGACCTCTTGAAGAAGCAGACTGACC 465
D 472 ACAAGAGAATCAGTGTCTGCTGACCTGTAGTTAAATTTTGAAGAACAACATCAT 531
QY 466 TGGAGAAAATGTCAAGAAAATATATGATCGGGCCCAAACTCTCTGTAATGTGAGCGCT 525
D 532 TAGAAGTAAATTTTGAAGAAAATAGTGTCCACATATATCTCTTTCATGCAAGTGCAGAAAT 591
QY 526 GTTCTGTTTACTCTAGAGACATCGAATACACAGTGGTCAAAATTTACCAAAATCCCTTG 585
D 592 GCACCAATTTTCTAGTGTGATGAAGATTGCTCCGATCTCTTTTCTAGTGTGTTTCCATG 651
QY 586 AATTGATGTCCTCCAAAGTGCAGTGTGATGTGAGAACAGTTTCAAGAAAAGCATGAGGA 645
D 652 AGTGTGAGGAATTAAGAAAATCATCTGATACATTAACAAGGGAACATGATCAACAAA 711
QY 646 AATCATCATCTCCGACTGGCTTAATAAATACAGCATTTGAGTGGTGTCTTCAACAG 705
D 712 TCAATTATCATGTATGCTCAGTATGTCAAAAATATCTATGGAACCACTTAATATCCAGATG 771
QY 706 GCCTTCCAGTGAACA-----TCAGTGTGCTTACCAGGATCCGCTTTGATGAGGCG 760
D 772 TCAGTAAAGTAAAGATTTCCTTGGACAACCTGAAAATACAGGAATGTAAACAGCAGT 831
QY 761 AGACCAGATATCTGTTTTCACATAAGATCTGTTCTTTGTGCTCCTATTTTGAATAGCAA 820
D 832 GCATTAGAAGTTGCTTTGTACACCTATAAAAATGGAAGAAGAAATTAATAGGG 891
QY 821 CCACCAATATTTGAGTGGCTCAAGTGTAAACAGACATTTGATGGGAACCTTTTGTATGA 880
D 892 TTTGCCAATCTGTTAATAAGATGAGGAGATACTGGC--AAGGTTAAGCCCTTTCAACCG 949
QY 881 TGCAGATCAACAGCTTTTGTAGGCTTTTGTATCTTTTGTGACTTGGCTGCAACAACAC 940
D 950 AAATGACGAACAGTTTCTGGAAGCTTTTGTATCTTTTGTGCTTGGGATGCCAGAAC 1009
QY 941 AATTATGATGATCAAGTGAAGAAGTCTCTGGCCCAAGCAGTCTGTGGCTCTTGTATGCT 1000
D 1010 GCAGATGTATGAAGCAGTGGAGAGGACCATGGCCCAAGCAAAATGCTCATTTGGAGTTCT 1069
QY 1001 ATCATACATCAACATGTTTCAAAAGCTGAAGTTGACAAGTTTGAAGGAGCCACATCC 1060
D 1070 GTCGTATCATCTTCAGCAGCAGGAGGAAGAAGAGAGCATAGACGTTAGCGGCTG 1129
QY 1061 TCTGGTGTGAC-----AATGTGCTATCGATGACATCATTTTGTGACTTTTCTCT 1111
D 1130 TGTGGTCCATCTGCCAGACCTTTAAATTTACTGACTTTTAGCTTCAGTCTTGAGCT 1189
QY 1112 CGAGTTGATGCCATGATCAAGCTGCTCTCCGATGTTTCATGGAGCTGGGATGTTACA 1171
D 1190 GTCTGATCTGAAACAGCAGCTGTACAAATTCGATGCTTTACTGACCTCAACCTTGTA 1249
QY 1172 GAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAACATGAGGAAAACATA 1231
D 1250 GAACCTCCAGATGAAACATGAGTGTGTTTTCAGATGAGATTTTAACTGTTAAGAGAATTA 1309
QY 1232 TCGGATG---GTTCTATACACAACACTGGAGACATGCTTCAACGCTGTGCTGAGTGT 1288
D 1310 TCGAAGATGTTGCCCTATCATAAATGGAGACATGCTTTTAAACACTCAGTGCATGTT 1369
QY 1289 CGGATGTTTAACCACTGCTGGTGTAAAGACATTTCTGACCGAGTGGAAATTTTAGCGGT 1348
D 1370 TGCTGCTTAAAGCAGGCAAAATTCAGAACAGCTGACCTGACCTGAGATGACTTGCATT 1429
QY 1349 GATTGTGGATGCTGTGTATGACCTCGACACAGGGGACCAACAAATGCTTCCAGC 1408
D 1430 GCTGATTGCTGCATAGGACACAGATTTGGATTCACCGTGTGTAATAACTCTTACATACA 1489
QY 1409 TAAGAGTGGCTTCTGCCCTGGCCCAACCTTATGGAACCTCTGCTACCTTGGAGCATCACCA 1468
D 1490 GCAGAGTGAACATCCACTTGCACAGCTTTACTG---CCATTCAATCATGGAACACCATCA 1546

QY 1469 TTTCAACACCGCGTGTATGATCTTTCAAGTGAAGGTCACAATATCTTGTCAACCTGTC 1528
D 1547 TTTTGACCACTGCGCTGATGATCTTTAATAGTCCAGCAATCAGATTCTCAGTGGCCTCTC 1606
QY 1529 TTTCAAGAAATATAGTGAACCTTATGACCTTTTGAAGCAGTCAATATTTGCAACAGACCT 1588
D 1607 CATTTGAAGAATATAGACCCAGCTTTGAAATTAATCAAGCAAGCTATTTTAGCTACAGACCT 1666
QY 1589 CACCTCTACTTTTCAGAGGAGAACTGAATCTTTTGAACCTTCTCAGTAAAGAGAAATACGA 1648
D 1667 AGCACTGTACATTAAGAGGCGAGGAGAAATTTTGAACCTTATAAGAAAAATCAATCAAA 1726
QY 1649 TTGGAACATCAAAACCATCTGATATATATTTTTCGATCAATGTTTATGACAGCTGTGACCT 1708
D 1727 TTTGGAAGATCTCATCAAAAGGAGTCTTTTGGCAATGCTGATGACAGCTTGTGATCT 1786
QY 1709 TGGAGCGTGTACCAAAACCGTGGGAGATCTCTCAGACAGTGGCAGAACTTTGTAACAGTGA 1768
D 1787 TTTGCAATTAACAAAACCTGGCCTATTTCAACAAGGATAGCAGAACTTTGAGCAACTGA 1846
QY 1769 GTTCTTTCAGAACAGGAGATCGGAGAGATTTAGACTCAAACTCACTCTTTCAGCAATTTT 1828
D 1847 ATTTTGTGATCAAGGAGAGAGAGAAAGAACTCAACATAGAACCCACTGATCTAAT 1906
QY 1829 TGATCGGAACCGGAGGATGAACCTCGCTCGGTTTCAACTGGAGTGGATTTGATAGCATCTG 1888
D 1907 GAACAGGAGAGAGAAACAAATCCCAAGTATGCAAGTTGGGTTTCATAGATGCCATCTG 1966
QY 1889 CATGCCCTTTGTATCAG 1904
D 1967 CTGCAACTGTATGAG 1982

RESULT 13

US-08-464-410A-12
; Sequence 12, Application US/08464410A
; Patent No. 6037119
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecik, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,410A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037119and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448

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; Sequence 12, Application PC/TUS9406066			
; GENERAL INFORMATION:			
; APPLICANT: The Board of Regents of the University of Washington			
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific			
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods			
; NUMBER OF SEQUENCES: 23			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &			
; ADDRESS: Borun			

[illegible]

GenCore version 5.1.6
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Run on: June 20, 2003, 18:30:48 ; Search time 324 Seconds

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Total number of hits satisfying chosen parameters: 2085038

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1664.8	80.1	2261	10	US-09-891-216-7
6	1503.8	72.4	1784	9	US-10-094-168B-2
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8	388.8	18.7	426	10	US-09-891-216-4
9	388.8	18.7	426	10	US-09-891-216-11
10	356.6	17.2	2645	9	US-10-115-515-22
11	345.2	16.6	1982	9	US-10-115-515-12
12	343.6	16.5	4474	9	US-10-115-515-9
13	219.2	10.5	2554	10	US-09-321-801-1
14	219.2	10.5	2798	10	US-09-321-801-3
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19	213.8	10.3	3044	10	US-09-883-825-44

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21	213.8	10.3	4240	9	US-09-954-531-971	Sequence 971, App
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25	181	8.7	3231	9	US-10-175-523-149	Sequence 149, App
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ALIGNMENTS

RESULT 1

US-09-891-216-8
; Sequence 8, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2502
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2502)
; OTHER INFORMATION: n = A,T,C or G
US-09-891-216-8

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Matches 2058;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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QY	66	AAAAGGTGAAATACAAAGACTGTCCAAATCTCTGGGGCTCTTTGGCTGAAAAACAG	125	
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; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221


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: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: PCT/EP01/07289
: PRIOR FILING DATE: 2001-06-26
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 2889
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-891-216-9

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Matches 1893; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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1549 TTATGACAGCTTTTGAAGCAGTCAATATTTGGCAACAGACTCAGCGTGTACTTTTGAGAGA 1608
2313 TTATGACAGCTTTTGAAGCAGTCAATATTTGGCAACAGACTCAGCGTGTACTTTTGAGAGA 2372
1609 GAACGTAAATTTTGAACCTTGTCAAGTAAAGAGAGATACGATTTGGAAACATCAAAACCATC 1668
2373 GAACGTAAATTTTGAACCTTGTCAAGTAAAGAGAGATACGATTTGGAAACATCAAAACCATC 2432
1669 GTGATATATTTTCGATCAATGTTTATGACAGCTGTGACCTTTGGAGCCGTGACCAACCGT 1728
2433 GTGATATATTTTCGATCAATGTTTATGACAGCTGTGACCTTTGGAGCCGTGACCAACCGT 2492
1729 GGGAGATCTCCAGACAGTGGCAGAACTTGTAAACAGTGAAGTCTTCCGAACAGGAGATC 1788
2493 GGGAGATCTCCAGACAGTGGCAGAACTTGTAAACAGTGAAGTCTTCCGAACAGGAGATC 2552
1789 GGGAGATCTCCAGACAGTGGCAGAACTTGTAAACAGTGAAGTCTTCCGAACAGGAGATC 1848
2553 GGGAGATCTCCAGACAGTGGCAGAACTTGTAAACAGTGAAGTCTTCCGAACAGGAGATC 2612
1849 AACTGCCCTCGGTTCGAACCTGGAGTGGATGATGATGATGATGATGATGATGATGATGATG 1908
2613 AACTGCCCTCGGTTCGAACCTGGAGTGGATGATGATGATGATGATGATGATGATGATGATG 2672
1909 TGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1968
2673 TGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2732
1969 AGTGGGAAGAGCTACACCAAAACAGCTGCTGGCCCTCAACTGCTTCACTCTCTCTCTCTCT 2028
2733 AGTGGGAAGAGCTACACCAAAACAGCTGCTGGCCCTCAACTGCTTCACTCTCTCTCTCTCT 2088
2029 CCAGTGGTATGGTAGCCCAAGGAGACAGGAATAA 2063
2793 CCAGTGGTATGGTAGCCCAAGGAGACAGGAATAA 2827

RESULT 3
US-09-891-216-18
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Query Match	91.0%;	Score 1891.8;	DB 10;	Length 2889;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1893;	Conservative	0;	Mismatches	2;
			Indels	0;
Qy	169	AGGATCGACGATTCAATGATGAAATCGACAAGCTGACTGTGATACAGACAAAAATCATTTAT	228	
Db	933	AGGATCGACGATTCAATGATGAAATCGACAAGCTAAGTGGATACAGACAAAAATCATTTAT	992	
Qy	229	TGTGCATGCTATCCGAAGCAGTGATGGTGAGATTATTGTTGTGGCCCAAGCGATAAATA	288	
Db	993	TGTGCATGCTATCCGAAGCAGTGATGGTGAGATTATTGTTGTGGCCCAAGCGATAAATA	1052	
Qy	289	AGATTCTCTGAAGCAGCTCCATTTACTTCAAGCATGATGAAAAAGTTATCCAGATGTATCTTC	348	
Db	1053	AGATTCTCTGAAGCAGCTCCATTTACTTCAAGCATGATGAAAAAGTTATCCAGATGTATCTTC	1112	
Qy	349	CATTTTTGTGGAATCGCCATATCTAAAGCTCAGCTCTTTGCTGGCTCAAGGAAAAAGATATG	408	
Db	1113	CATTTTTGTGGAATCGCCATATCTAAAGCTCAGCTCTTTGCTGGCTCAAGGAAAAAGATATG	1172	
Qy	409	AAGAAGCAGAGCTTTGCTAGAGGTGGTTAATGACCTCTTTGAAGAACACACATGACCTGG	468	
Db	1173	AAGAAGCAGAGCTTTGCTAGAGGTGGTTAATGACCTCTTTGAAGAACACACATGACCTGG	1232	
Qy	469	AGAAAAATTGCAAGAAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGFGAGCGGTGTT	528	
Db	1233	AGAAAAATTGCAAGAAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGFGAGCGGTGTT	1292	
Qy	529	CTGTTTACTTCCCTAGAGGACATCGAATCACAGTGGTGAATTTACCAAACTCTTTGAAT	588	
Db	1293	CTGTTTACTTCCCTAGAGGACATCGAATCACAGTGGTGAATTTACCAAACTCTTTGAAT	1352	
Qy	589	TGATGTCGCCAAAGTCAGTGCCTGATCGTGCAGAACAGTTTCAAGAAAGCATGGAGAAAT	648	
Db	1353	TGATGTCGCCAAAGTCAGTGCCTGATCGTGCAGAACAGTTTCAAGAAAGCATGGAGAAAT	1412	
Qy	649	CATCATACTCCGACTGGCTAATAAATAACAGCATTTGCTGAGCTGGTGTCTTCAACAGGCC	708	
Db	1413	CATCATACTCCGACTGGCTAATAAATAACAGCATTTGCTGAGCTGGTGTCTTCAACAGGCC	1472	
Qy	709	TTCCAGTGAACATCAGTGATGCCCTACCAGATCCGGCGCTTTGATGCAGAGGCAGACCAGA	768	
Db	1473	TTCCAGTGAACATCAGTGATGCCCTACCAGATCCGGCGCTTTGATGCAGAGGCAGACCAGA	1532	
Qy	769	TATCTGGTTTTCACATAAGATCTGTTCTTTGCTGCTCTATTTTCCGATAGCAACACCCAAA	828	
Db	1533	TATCTGGTTTTCACATAAGATCTGTTCTTTGCTGCTCTATTTTCCGATAGCAACACCCAAA	1592	
Qy	829	TAATTGGAGTGGCTCAAGTGTTAACAGACTTGTATGGGAACCTTTTGTATGTATGCAGATC	888	

Qy	1969	AGTGGGAAGAGCTACACCAAAAAACGACTGCTGCCCTCAACTGCCTCATCTCTCTCCCTG	2028
Db	2733	AGTGGGAAGAGCTACACCAAAAAACGACTGCTGCCCTCAACTGCCTCATCTCTCCCTG	2792
Qy	2029	CCAGTGTATTGTGTAGCCAGGAAGACAGGAACATAA	2063
Db	2793	CCAGTGTATTGTGTAGCCAGGAAGACAGGAACATAA	2827

Query Match	91.08;	Score 1891.8;	DB 10;	Length 4656;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1893;	Conservative	0;	Mismatches	2;
			Indels	0;
Qy	169	AGGATCGACCATCAATGATCAATCGACAAGCTGACTGCATCAAGACAAAAATCATTAT	228	
Db	1409	AGGATCGACCATCAATGATCAATCGACAAGCTGACTGCATCAAGACAAAAATCATTAT	1468	
Qy	229	TGTGTCATGCCATATCCGAAGCAGTGATGGTGCAGATTATTGGTGTGGCCCAAGCGATAAATA	288	
Db	1469	TGTGTCATGCCATATCCGAAGCAGTGATGGTGCAGATTATTGGTGTGGCCCAAGCGATAAATA	1528	
Qy	289	AGATTCTCGAAGGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTTTC	348	
Db	1529	AGATTCTCGAAGGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTTTC	1588	
Qy	349	CATTTTGTGGAATGCCATATCTAAGCGCTCAGCTCTTTTGTGCGCTCAAGGAAAGAATATG	408	
Db	1589	CATTTTGTGGAATGCCATATCTAAGCGCTCAGCTCTTTTGTGCGCTCAAGGAAAGAATATG	1648	
Qy	409	AAAGAAGCAGAGCTTTGCTAGAGGTGGTTAATGACCTCTTTTGAAGAACACAGCTGACCTGG	458	
Db	1649	AAAGAAGCAGAGCTTTGCTAGAGGTGGTTAATGACCTCTTTTGAAGAACACAGCTGACCTGG	1708	
Qy	469	AGAAATTTGTCAAGAAATAATCATCGCGGCCCAAACTCTGCTCAATGTGACGGCTGTT	528	
Db	1709	AGAAATTTGTCAAGAAATAATCATCGCGGCCCAAACTCTGCTCAATGTGACGGCTGTT	1768	
Qy	529	CTGTTTTTACTCCTAGAGGACATCGAATCACAGTGGTGAATTTTACCAAAATCCTTTGAAT	588	
Db	1769	CTGTTTTTACTCCTAGAGGACATCGAATCACAGTGGTGAATTTTACCAAAATCCTTTGAAT	1828	
Qy	589	TGATGTCCCAAAAGTGCAGTGCCTGATGCTGAGAACAGTTTCAAGAAAGCATGGAGAAAT	648	
Db	1829	TGATGTCCCAAAAGTGCAGTGCCTGATGCTGAGAACAGTTTCAAGAAAGCATGGAGAAAT	1888	
Qy	649	CATCATATCTCCGACTGGCTTAATAATAACAGCAATGCTGAGCTGGTTGCTTCAACAGGCC	708	

Qy 1706 CTTTGGAGCCGTGACCAAAACCGTGGGAGATCTCAGACAGGTGCGAGAACTTGTAAACCAG 1765
Db 1539 CTTTGGAGCCGTGACCAAAACCGTGGGAGATCTCAGACAGGTGCGAGAACTTGTAAACCAG 1598
Qy 1766 TGAGTCTCTCGAAACGAGATCGGAGAGATTAGAGCTCAAACTCACTCCTTCAGCAAT 1825
Db 1599 TGAGTCTCTCGAAACGAGATCGGAGAGATTAGAGCTCAAACTCACTCCTTCAGCAAT 1658
Qy 1826 TTTTGTATCGGAACCGGAGATGAACCTGCCCTGCTTGCACCTGGAGTGGATTGATAGCAT 1885
Db 1659 TTTTGTATCGGAACCGGAGATGAACCTGCCCTGCTTGCACCTGGAGTGGATTGATAGCAT 1718
Qy 1886 CTGCATGCGCTTTGTATCAGGCACCTGGTGAAGGTCAACGTGAACTGAAAGCCGATGCTTAGA 1945
Db 1719 CTGCATGCGCTTTGTATCAGGCACCTGGTGAAGGTCAACGTGAAAGCCGATGCTTAGA 1778
Qy 1946 TTCACTAGCTACAACAGAGTAAGTGGGAGAGCTACACCAAAAACGACTGCTGGCCTC 2005
Db 1779 TTCACTAGCTACAACAGAGTAAGTGGGAGAGCTACACCAAAAACGACTGCTGGCCTC 1838
Qy 2006 AACTGCCCTCATCTCCCTCCCTGCCAGTGTATGGTAGCCCAAGGAAGACAGAACTAA 2063
Db 1839 AACTGCCCTCATCTCCCTCCCTGCCAGTGTATGGTAGCCCAAGGAAGACAGAACTAA 1896

RESULT 6

US-10-094-168B-2
; Sequence 2, Application us/10094168B
; Publication No. US20030092156A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.; Harrow, Ian
; APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-2 CIP
; CURRENT APPLICATION NUMBER: US/10/094.168B
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1784
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A1
US-10-094-168B-2

Query Match 72.4%; Score 1503.8; DB 9; Length 1784;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 557 ACCAGTGGTGAATTTACCAATCCTTTGAATTTGATGTGCCCAAGTGCAGTGCATGATGC 616
Db 117 ACAGTGGTGAATTTACCAATCCTTTGAATTTGATGTGCCCAAGTGCAGTGCATGATGC 176
Qy 617 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA 676
Db 177 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA 236
Qy 677 CAGCATTTGCTGAGCTGGTGTGCTCAACAGGCCCTTCCAGTGAACATCAGTGTGCTTACCA 736
Db 237 CAGCATTTGCTGAGCTGGTGTGCTCAACAGGCCCTTCCAGTGAACATCAGTGTGCTTACCA 296
Qy 737 GGATCCGCGCTTTGATGACAGAGGACACAGATATCTGGTTTTTACATAAAGATCTGTCT 796
Db 297 GGATCCGCGCTTTGATGACAGAGGACACAGATATCTGGTTTTTACATAAAGATCTGTCT 356

Qy 797 TTGTGTCCTTATTTGGGAATAGCAACCAACCAAAATAAATTGGAGTGGCTCAAGTGTAAACAG 856
Db 357 TTGTGTCCTTATTTGGGAATAGCAACCAACCAAAATAAATTGGAGTGGCTCAAGTGTAAACAG 416
Qy 857 ACTTGTATGGGAAACCTTTTGTATGATGAGATCAACGACTTTTTCGAGCTTTTGTGCATCTT 916
Db 417 ACTTGTATGGGAAACCTTTTGTATGATGAGATCAACGACTTTTTCGAGCTTTTGTGCATCTT 476
Qy 917 TTGTGGACTTTGGCATCAACACACAATATATGATGATCAAGTGAAGAAGTCTCTGGGCCAA 976
Db 477 TTGTGGACTTTGGCATCAACACACAATATATGATGATCAAGTGAAGAAGTCTCTGGGCCAA 536
Qy 977 GCACTCTGTGCTCTTGTATGCTATCATACCATGCAACATGTTCAAAAGCTGAAGTTGA 1036
Db 537 GCACTCTGTGCTCTTGTATGCTATCATACCATGCAACATGTTCAAAAGCTGAAGTTGA 596
Qy 1037 CAAGTTTAAAGCAGCAGCAACATCCCTCTGGTGTCAAGACTTCCCATCGATGACATTCATTT 1096
Db 597 CAAGTTTAAAGCAGCAGCAACATCCCTCTGGTGTCAAGACTTCCCATCGATGACATTCATTT 656
Qy 1097 TGATGACTTTTCTCTCGACGTTGATGCGCATGATCACAGCTGCTCTCCGGATGTTTCATGGA 1156
Db 657 TGATGACTTTTCTCTCGACGTTGATGCGCATGATCACAGCTGCTCTCCGGATGTTTCATGGA 716
Qy 1157 GCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC 1216
Db 717 GCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC 776
Qy 1217 AGTGAGGAAAACATATCGGATGTTTCAACACACTGCTGGGTTTCAAGACATTTTCACCGAGTGA 1276
Db 777 AGTGAGGAAAACATATCGGATGTTTCAACACACTGCTGGGTTTCAAGACATTTTCACCGAGTGA 836
Qy 1277 TCAGCTGATGTTCCGCGATGTTAAACACACTGCTGGGTTTCAAGACATTTTCACCGAGTGA 1336
Db 837 TCAGCTGATGTTCCGCGATGTTAAACACACTGCTGGGTTTCAAGACATTTTCACCGAGTGA 896
Qy 1337 AATTTTAGCGTGATGTTGGGATGCCGTGTGTCATGACCTCGACACAGGGGAACCAACAA 1396
Db 897 AATTTTAGCGTGATGTTGGGATGCCGTGTGTCATGACCTCGACACAGGGGAACCAACAA 956
Qy 1397 TGCCTTCAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATGCAACTCTGCTACCTT 1456
Db 957 TGCCTTCAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATGCAACTCTGCTACCTT 1016
Qy 1457 GGAGCATCACCATTTCACACACGCGGTGATGATCCTTCAAAAGTGAAGGTCAACAATATCTT 1516
Db 1017 GGAGCATCACCATTTCACACACGCGGTGATGATCCTTCAAAAGTGAAGGTCAACAATATCTT 1076
Qy 1517 TGCTAACTGTCTCCCAAGGAATATAGTGACCTTTATGACAGCTTTTGAAGCAGTCAATAT 1576
Db 1077 TGCTAACTGTCTCCCAAGGAATATAGTGACCTTTATGACAGCTTTTGAAGCAGTCAATAT 1136
Qy 1577 GGCAACAGACCTCAGCTGTACTTTTGAGAGAGAGTGAATTTCTTTGAACCTTGACGTAA 1636
Db 1137 GGCAACAGACCTCAGCTGTACTTTTGAGAGAGAGTGAATTTCTTTGAACCTTGACGTAA 1196
Qy 1637 AGGAGATACCATTTGGAACATCAAAACCATCTCGTATATTTTCGATCAATGTTTAATGAC 1696
Db 1197 AGGAGATACCATTTGGAACATCAAAACCATCTCGTATATTTTCGATCAATGTTTAATGAC 1256
Qy 1697 AGCCTGTGACCTTGGAGCCGTGACCAACCGTGGAGATCTCCACAGAGTGGCAGAACT 1756
Db 1257 AGCCTGTGACCTTGGAGCCGTGACCAACCGTGGAGATCTCCACAGAGTGGCAGAACT 1316
Qy 1757 TGTAAACAGTTCAGTCTTCGAAACAGGAGATCGGGAGAGATTAGAGCTCAAACTCAGTCC 1816
Db 1317 TGTAAACAGTTCAGTCTTCGAAACAGGAGATCGGGAGAGATTAGAGCTCAAACTCAGTCC 1376
Qy 1817 TTCAGCAATTTTTCATCGGAACCGGAGATGAACTGCCTCGTTCGCTTGAACCTGGAGTGGAT 1876
Db 1377 TTCAGCAATTTTTCATCGGAACCGGAGATGAACTGCCTCGTTCGCTTGAACCTGGAGTGGAT 1436
Qy 1877 TGATAGCATCTGCATGCTTTTGTATCAGGCACTGGTGAAGGTCAACGCTGAACCTGAAGCC 1936

Db 1437 TGATAGCATCTGCATGCCCTTTGTATCAGGCACCTGGTGAAGGTCAACGTGAAGCC 1496
QY 1937 GATGCTAGATTCAGTAGCTACAAACAGAAAGTAAGTGGGAAGAGCTACACCAAAACAGACT 1996
Db 1497 GATGCTAGATTCAGTAGCTACAAACAGAAAGTAAGTGGGAAGAGCTACACCAAAACAGACT 1556
QY 1997 GCTGCCCTCAACTGCCTCATCTCTCCCTGCCAGTCTTATGGTAGCAAGGAAGACAG 2056
Db 1557 GCTGCCCTCAACTGCCTCATCTCTCCCTGCCAGTCTTATGGTAGCAAGGAAGACAG 1616
QY 2057 GAACTAA 2063
Db 1617 GAACTAA 1623

RESULT 7

US-10-094-168B-4
; Sequence 4, Application US/10094168B
; Publication No. US20030092156A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.; Harrow, Ian
; APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-2 CIP
; CURRENT APPLICATION NUMBER: US/10/094,168B
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1982
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDEL0A2
US-10-094-168B-4

Query Match 50.3%; Score 1045.6; DB 9; Length 1982;

Best Local Similarity 99.6%; Pred. No. 7,le-315;

Matches 1048; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 557 ACCAGTGTGAAATTTACCAATCCTTTGAATTCATGTCCTCCCAAGTGCAGTGTGATGC 616
Db 123 ACAGTGTGAAATTTACCAATCCTTTGAATTCATGTCCTCCCAAGTGCAGTGTGATGC 182
QY 617 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA 676
Db 183 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA 242
QY 677 CAGATTGCTGAGCTGGTTGCTTCAACAGGCTTCCAGTGAACATCAGTATGCTACCA 736
Db 243 CAGATTGCTGAGCTGGTTGCTTCAACAGGCTTCCAGTGAACATCAGTATGCTACCA 302
QY 737 GGATCCGCGCTTTGATGAGAGGAGCAGACATATCTGTTTTCACATAAGATCTGTCT 796
Db 303 GGATCCGCGCTTTGATGAGAGGAGCAGACATATCTGTTTTCACATAAGATCTGTCT 362
QY 797 TTGTGCTCCTATTGGGAATAGCACCACCAATTAATGGAGTGGCTCAAGTGTAAACAG 856
Db 363 TTGTGCTCCTATTGGGAATAGCACCACCAATTAATGGAGTGGCTCAAGTGTAAACAG 422
QY 857 ACTTGATGGGAACCTTTTGTATGATGAGATCAACAGACTTTTTTGAGGCTTTTGTCACTCT 916
Db 423 ACTTGATGGGAACCTTTTGTATGATGAGATCAACAGACTTTTTTGAGGCTTTTGTCACTCT 482
QY 917 TTGTGAGCTTGGCATCAACACAAATATGATCAAGTGAAGAGTCTCTGGGCCAA 976

Db 483 TTGTGAGCTTGGCATCAACAAACAAATATGATGATCAAGTGAAGAGTCTCTGGGCCAA 542
QY 977 GCAGTCTGTGCTCTTGTATGATGCTATCATACCATGCAACATGTTCAAAAGCTGAAGTTGA 1036
Db 543 GCAGTCTGTGCTCTTGTATGATGCTATCATACCATGCAACATGTTCAAAAGCTGAAGTTGA 602
QY 1037 CAAAGTTTAAAGCAGCAACATCCCTCTCTGTTGTCAGAACTTGCATCGATGACATTCATTT 1096
Db 603 CAAAGTTTAAAGCAGCAACATCCCTCTCTGTTGTCAGAACTTGCATCGATGACATTCATTT 662
QY 1097 TGATGACTTTTCTCTCGACGTTGATGCGCATGATCAGAGCTCTCTCCGGATGTTTCATGGA 1156
Db 663 TGATGACTTTTCTCTCGACGTTGATGCGCATGATCAGAGCTCTCTCCGGATGTTTCATGGA 722
QY 1157 GCTGGGATGTTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTTCAC 1216
Db 723 GCTGGGATGTTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTTCAC 782
QY 1217 AGTGAGGAAAAATATCGGATGGTTCATACCAACATGGAGACATGCTTCAACGTGTG 1276
Db 783 AGTGAGGAAAAATATCGGATGGTTCATACCAACATGGAGACATGCTTCAACGTGTG 842
QY 1277 TCAGTGTATGTCGCGATGTTAAACACATGCTGGGTTTCAAGACATTCATGACCGAGTGA 1336
Db 843 TCAGTGTATGTCGCGATGTTAAACACATGCTGGGTTTCAAGACATTCATGACCGAGTGA 902
QY 1337 AATTTAGCGGTGATGTTGGGATGCCCTGTGTCATGACCTCGACACACAGGGGAACCAAA 1396
Db 903 AATTTAGCGGTGATGTTGGGATGCCCTGTGTCATGACCTCGACACACAGGGGAACCAAA 962
QY 1397 TGCCTTCCAAAGCTAAGAGTGGCTCTGCTCCCTGGCCCAACTCTATGAACTCTGCTACCTT 1456
Db 963 TGCCTTCCAAAGCTAAGAGTGGCTCTGCTCCCTGGCCCAACTCTATGAACTCTGCTACCTT 1022
QY 1457 GGAGCATCACATTTCAACACACGCGGTGATGATCCTTCAAAGTGAAGGTGAGGTACAATATCTT 1516
Db 1023 GGAGCATCACATTTCAACACACGCGGTGATGATCCTTCAAAGTGAAGGTGAGGTACAATATCTT 1082
QY 1517 TGCTAACCTGTCTCCCAAGGAATATAGTGACCTTATGACGCTTTTGAGCAGTCAATATT 1576
Db 1083 TGCTAACCTGTCTCCCAAGGAATATAGTGACCTTATGACGCTTTTGAGCAGTCAATATT 1142
QY 1577 GGCAACAGACCTCACGCTGTACTTTGAGAGGA 1608
Db 1143 GGCAACAGACCTCACGCTGTACTTTGAGAGGA 1174

RESULT 8

US-09-891-216-4
; Sequence 4, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973 00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-891-216-4

Query Match 18.7%; Score 388.8; DB 10; Length 426;

Best Local Similarity 99.5%; Pred. No. 1.6e-110;
Matches 390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 171 GATCGACGATCAATGATGAATGCAAGCTGACTGGATACAGACAAAATCATTTG 230
Db 1 CATCGACGATCAATGATGAATGCAAGCTGACTGGATACAGACAAAATCATTTG 60
QY 231 TGCATGCTATCCGAAGCAGTGATGGTGAGATTATTTGGTGGCCCAAGCGATAAATAAG 290
Db 61 TGCATGCTATCCGAAGCAGTGATGGTGAGATTATTTGGTGGCCCAAGCGATAAATAAG 120
QY 291 ATTCTGAAGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTTCCA 350
Db 121 ATTCTGAAGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTTCCA 180
QY 351 TTTTGTGGAATCGCCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAAGATATGAA 410
Db 181 TTTTGTGGAATCGCCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAAGATATGAA 240
QY 411 AGAAGCAGAGCTTTGCTAGAGTGGTTAATGACCTCTTTGAAGACAGACTGACCTGGAG 470
Db 241 AGAAGCAGAGCTTTGCTAGAGTGGTTAATGACCTCTTTGAAGACAGACTGACCTGGAG 300
QY 471 AAAATTGTCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGAGCGCTGTCT 530
Db 301 AAAATTGTCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGAGCGCTGTCT 360
QY 531 GTTTTACTCTTAGAGGACATCGAATCACCAGT 562
Db 361 GTTTTACTCTTAGAGGACATCGAATCACCAGT 392
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RESULT 9

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US-09-891-216-11
; Sequence 11, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-891-216-11
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Query Match 18.7%; Score 388.8; DB 10; Length 426;
Best Local Similarity 99.5%; Pred. No. 1.6e-110;
Matches 390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 171 GATCGACGATCAATGATGAATGCAAGCTGACTGGATACAGACAAAATCATTTG 230
Db 1 GATCGACGATCAATGATGAATGCAAGCTGACTGGATACAGACAAAATCATTTG 60
QY 231 TGCATGCTATCCGAAGCAGTGATGGTGAGATTATTTGGTGGCCCAAGCGATAAATAAG 290
Db 61 TGCATGCTATCCGAAGCAGTGATGGTGAGATTATTTGGTGGCCCAAGCGATAAATAAG 120
QY 291 ATTCTGAAGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTTCCA 350
Db 121 ATTCTGAAGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTTCCA 180
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QY 351 TTTTGTGGAATCGCCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAAGATATGAA 410
Db 181 TTTTGTGGAATCGCCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAAGATATGAA 240
QY 411 AGAAGCAGAGCTTTGCTAGAGTGGTTAATGACCTCTTTGAAGACAGACTGACCTGGAG 470
Db 241 AGAAGCAGAGCTTTGCTAGAGTGGTTAATGACCTCTTTGAAGACAGACTGACCTGGAG 300
QY 471 AAAATTGTCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGAGCGCTGTCT 530
Db 301 AAAATTGTCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGAGCGCTGTCT 360
QY 531 GTTTTACTCTTAGAGGACATCGAATCACCAGT 562
Db 361 GTTTTACTCTTAGAGGACATCGAATCACCAGT 392
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RESULT 10

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US-10-115-515-22
; Sequence 22, Application US/10115515
; Publication No. US20030054992A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Corbin, Jackie D.
; Ferguson, Kenneth M.
; Francis, Sharron H.
; Kadlec, Ann
; Loughney, Kate
; McAllister-Lucas, Linda M.
; Sonnenburg, William K.
; Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/10/115,515
; APPLICATION NUMBER: US/10/115,515
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/599,658
; FILING DATE: 21-Jun-2000
; APPLICATION NUMBER: 09/055,584
; FILING DATE: 4-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030054992A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2645 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 12..2636
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GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
Corbin, Jackie D.
Ferguson, Kenneth M.
Francis, Sharron H.
Kadlecek, Ann
Loughney, Kate
McAllister-Lucas, Linda M.
Sonnenburg, William K.
Thomas, Melissa K

Db 1705 CTGTGGTACCATCTGCCGAGACCCCTTAAATCACTGACTTCAGCTTCAGCGACTTTTGAGC 1764
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Qy 1948 CAGTAGCTACAAACAGAGTAGTGAAGTGGAGAGCT 1981
Db 2602 GCTGAGAAAGAACAGGAGAGAAATGGCAGGCTCT 2635

RESULT 13

US-09-321-801-1
; Sequence 1, Application US/09321801
; Patent No. US20020115176A1
; GENERAL INFORMATION:
; APPLICANT: Lanfear, Jeremy
; APPLICANT: Robas, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMS
; FILE REFERENCE: PC9477A
; CURRENT APPLICATION NUMBER: US/09/321.801

; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 9826777.6
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 9823882.7
; EARLIER FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 9811500.9
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 9908247.1
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 9910801.1
; EARLIER FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2554
; TYPE: DNA
; ORGANISM: Human
US-09-321-801-1

Query Match 10.5%; Score 219.2; DB 10; Length 2554;
Best Local Similarity 50.8%; Pred. No. 4.7e-57;
Matches 667; Conservative 0; Mismatches 623; Indels 24; Gaps 5;
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Qy 1268 CAACGTGTGCTGATGTTTCCGCGATGTTAACTGTTAACTGCTGCTGCTTCAAGACATTCAC 1327
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RESULT 14

US-09-321-801-3
; Sequence 3, Application US/09321801
; Patent No. US20020115176A1
; GENERAL INFORMATION:
; APPLICANT: Lanfear, Jeremy
; APPLICANT: Robas, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC9477A
; CURRENT APPLICATION NUMBER: US/09/321.801
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 9826777.6
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 9823882.7
; EARLIER FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 9811500.9
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 9908247.1
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 9910801.1
; EARLIER FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 2798
; TYPE: DNA
; ORGANISM: Human
US-09-321-801-3

Query Match 10.5%; Score 219.2; DB 10; Length 2798;
Best Local Similarity 50.8%; Pred. No. 5.1e-57;
Matches 667; Conservative 0; Mismatches 623; Indels 24; Gaps 5;
Qy 668 AATAAATAACAGCATTTGCTGAGCTGGTTCGCTTCAACAGGCGCTTCCAGTGAACATCACTGTA 727

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Db 1322 TGCCTATGACAGCAGCAGCTTTTAAACAGAGAGTAGAGCTTTGACAGAGCTACACACCGC 1381
Qy 788 ATCTGTTCTTTGTGCTCCCTATTTGGAATAGCAACCAACCAAAATTAATTTGAGTGGCTCAAGT 847
Db 1382 GAACATCCTGTGCATGCCCTCGTCAGCGGAGGAGCGTGATA---GGTGTGGTGCAGAT 1438
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Db 2498 CACGGAGCCTCTTCTGAAAGCATGCAGGGATAATCTCAGTCAGTGGGGAAGGT 2551

RESULT 15
US-09-420-190-2
; Sequence 2, Application US/09420190
; Patent No. US20020081633A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide Phosphodiesterase
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 4381
; TYPE: DNA.
; ORGANISM: Homo sapiens.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)...(2403)
US-09-420-190-2

Query Match 10.5% Score 217.6; DB 10; Length 4381;
Best Local Similarity 50.7%; Pred. No. 2.2e-56;
Matches 666; Conservative 0; Mismatches 624; Indels 24; Gaps 5;

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Db 2157 AATACAGCCTTATCTCTATGATGGACAGACAGAAGGATGAAGTCCCCCAAGGCCAGCT 2216
Qy 1868 GGAGTGGATTTGATAGCATCTGACCTTTGTATCAGGCACTGTTGAAGGTCAACGTGAA 1927
Db 2217 TGGGTTCTACAATGCCGTGGCCATTTCCCTGCTATACAACCTTACCAGATCTCCCTCC 2276
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:44:04 ; Search time 45.1845 Seconds
(without alignments)
3119.127 Million cell updates/sec

Title: US-09-663-542-1
Perfect score: 3516
Sequence: 1 MLKQARRPLFRNVLSTQWK.....ASTASSSPASVMVAKEDRN 684

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Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organella.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3354	95.4	988	Q96S76	Q96S76 homo sapien
3	3294.5	93.7	685	Q8VID7	Q8VID7 rattus norv
4	3250	92.4	934	Q9HCR9	Q9HCR9 homo sapien
5	3117.5	88.7	935	Q8VID6	Q8VID6 rattus norv
6	2970	84.5	576	Q9HB46	Q9HB46 homo sapien
7	2845.5	80.9	581	Q8VID8	Q8VID8 rattus norv
8	2541	72.3	490	Q9NY45	Q9NY45 homo sapien
9	1511.5	43.0	1284	Q9VJ79	Q9VJ79 drosophila
10	1478	42.0	1018	Q95TW8	Q95TW8 drosophila
11	1380.5	39.3	1232	Q9VFI9	Q9VFI9 drosophila
12	1054.5	30.0	861	Q91ZQ1	Q91ZQ1 mus musculu
13	1021	29.0	857	Q8UUY6	Q8UUY6 rana pipien
14	1019.5	28.0	861	Q8UUY5	Q8UUY5 rana pipien
15	1017	28.9	866	Q8UUY7	Q8UUY7 rana pipien
16	998	28.4	856	Q9MYV0	Q9MYV0 canis faml

ALIGNMENTS

RESULT 1

ID	Q9GZY7	PRELIMINARY;	PRT;	684 AA.
AC	Q9GZY7;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	CAMP/cgmp cyclic nucleotide phosphodiesterase 11A3 (Phosphodiesterase 11A2).			
GN	PDE11A3 OR HSPDE11A.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20524097; PubMed=11050148;			
RA	Hetman J.M., Robas N.M., Baxendale R., Fidock M., Phillips S.C.,			
RA	Soderling S.H., Beavo J.A.;			
RT	"Cloning and characterisation of two splice variants of human phosphodiesterase 11A.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TESTIS;			
RX	MEDLINE=20469516; PubMed=10906126;			
RA	Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;			
RT	"Isolation and Characterization of Two Novel Phosphodiesterase PDE11A Variants Showing Unique Structure and Tissue-specific Expression.";			
RL	J. Biol. Chem. 275:31469-31479(2000).			
DR	EMBL; AJ278682; CAC15567.1; -			
DR	EMBL; AB038041; BAB16372.1; -			
DR	InterPro; IPR003018; GAF.			
DR	InterPro; IPR003607; ME_Pplase_HDC.			
DR	InterPro; IPR002073; PDEase.			
DR	Pfam; PF01590; GAF; 2.			
DR	Pfam; PF00233; PDEase; 1.			
DR	PRINTS; PR00387; PDIESTERASE1.			
DR	SMART; SM00065; GAF; 2.			

Q62037 mus musculu
Q8R0D4 mus musculu
Q9NTV4 homo sapien
Q9HCP9 homo sapien
Q9ULW9 homo sapien
Q96076 ephydattia f
Q9WV11 mus musculu
Q9QYJ5 rattus norv
Q9QYJ6 rattus norv
Q9GQU6 trypanosoma
Q8WQX9 trypanosoma
Q97746 canis faml
Q9GTH9 trypanosoma
Q9QWH9 rattus norv
Q8QZV1 rattus norv
Q76105 homo sapien
Q84849 homo sapien
Q9UPJ5 homo sapien
Q43850 homo sapien
P78505 homo sapien
Q9EQR7 rattus norv
Q8R078 mus musculu
Q9H3H2 homo sapien
Q89084 mus musculu
Q35470 rattus norv
Q9VKE9 drosophila
P94181 anabaena sp
Q8SXR0 drosophila
Q8VIE3 rattus norv


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Db      541 NISDAYQDPRDAEQDISGPHIRSVLCVPTWNSNHQIIGVAQVNLRLDGPFDADQRL 600
Qy      297 FEAFFVFCGLGINNTIMYDQVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLYSEL 356
Db      601 FEAFFVFCGLGINNTIMYDQVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLYSEL 660
Qy      357 AIDDIHDDFSLVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLYHNW 416
Db      661 AIDDIHDDFSLVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLYHNW 720
Qy      417 RHAFNVCOLMFAMLTAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSALAOL 476
Db      721 RHAFNVCOLMFAMLTAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSALAOL 780
Qy      477 YGTSATLEHHFHNHAFVMILOSSEGHNIFANLSSKEYSDLMOLLKOSILATDILTYFERTE 536
Db      781 YGTSATLEHHFHNHAFVMILOSSEGHNIFANLSSKEYSDLMOLLKOSILATDILTYFERTE 840
Qy      537 FFELVSKGEYDWNKFNHRDIPRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEQGDRER 596
Db      841 FFELVSKGEYDWNKFNHRDIPRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEQGDRER 900
Qy      597 LELKLTSAIDRNRKDELPRLOLEWIDSICMPLYQALVKVNVKLKPMLDVATNRSKWE 656
Db      901 LELKLTSAIDRNRKDELPRLOLEWIDSICMPLYQALVKVNVKLKPMLDVATNRSKWE 960
Qy      657 ELHQKRLLASTASSSSPASVMVAKEDRN 684
Db      961 ELHQKRLLASTASSSSPASVMVAKEDRN 988

RESULT 3
Q8VID7 ID Q8VID7 PRELIMINARY; PRT; 685 AA.
AC Q8VID7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A3.
GN RNPDE11A3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohguru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
(PDE11A): comparison of rat and human PDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL; AB059361; BAB79628.1; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 685 AA; 78067 MW; 505E8748E9A6C21F CRC64;

Query Match          93.7%; Score 3294.5; DB 11; Length 685;
Best Local Similarity 93.7%; Pred. No. 1.le-236;
Matches 644; Conservative 13; Mismatches 23; Indels 7; Gaps 2;

Qy      1 MLKQARRPLFRNVLSATQWKVKITRLVQISGASLAEKQKHQDFLIQRTKTKDRFRND 60
Db      1 MLKQARRFSPNVRSAQWRKVGSTROGQISGAFLAERLKHQDFLFRMQTTRTKDRFRND 60
Qy      61 EIDLKTYGKTKSLCLMCPIRSSDGEIIGVAQAINKVPEGAPFTEDEKVMQMYLPFCGIAI 120

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Db      61 EIDLKTYGKTKSLCLMCPIRNSDGEIIGVAQAINKVPEGAPFTEDEKVMQMYLPFCGIAI 120
Qy      121 SNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCCERCSVLLLED 180
Db      121 SNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCCERCSVLLLED 180
Qy      181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNNSIAELVASTGLPVNISD 240
Db      181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNNSIAELVASTGLPVNISD 240
Qy      241 AYQDPRDAEQDISGPHIRSVLCVPTWNSNHQIIGVAQVNLRLDGPFDADQRLPEAF 300
Db      241 AYQDPRDAEQDISGPHIRSVLCVPTWNSNHQIIGVAQVNLRLDGPFDADQRLPEAF 300
Qy      301 VIFGCLGINNTIMYDQVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLYSELAIDD 360
Db      301 VIFGCLGINNTIMYDQVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLYSELAIDD 360
Qy      361 IHFDDFSLVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLYHNHRHAF 420
Db      361 IHFDDFSLVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLYHNHRHAF 420
Qy      421 NVCOLMFAMLTAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSALAOLYCTS 480
Db      421 NVCOLMFAMLTAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSALAOLYCTS 480
Qy      481 ATLEHHFHNHAFVMILOSSEGHNIFANLSSKEYSDLMOLLKOSILATDILTYFERTEFFEL 540
Db      481 ATLEHHFHNHAFVMILOSSEGHNIFANLSSKEYSDLMOLLKOSILATDILTYFERTEFFEL 540
Qy      541 VSKGEYDWNKFNHRDIPRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLEK 600
Db      541 VSKGAYDWSITSHRDVFRSMLTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERSELK 600
Qy      601 LTPSAIDRNRKDELPRLOLEWIDSICMPLYQALVKVNVKLKPMLDVATNRSKWEELHQ 660
Db      601 LTPSAIDRNRKDELPRLOLEWIDSICMPLYQALVKVNVKLKPMLDVATNRSKWEELHQ 660
Qy      661 KRLLASTA----SSSSPASVMVAKEDR 683
Db      661 KRLOVSAASPVSPSPSPA---VAGEDR 684

RESULT 4
Q9HCR9 ID Q9HCR9 PRELIMINARY; PRT; 934 AA.
AC Q9HCR9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A (Phosphodiesterase 11A4).
GN HSPDE11A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=20469516; PubMed=10906126;
RA Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
RT "Isolation and Characterization of Two Novel Phosphodiesterase PDE11A
Variants Showing Unique Structure and Tissue-specific Expression.";
RL J. Biol. Chem. 275:31459-31479(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570133; PubMed=11121118;
RA Yuasa K., Kanoh Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase PDE11A gene:
Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB036704; BAB16371.1; -.
DR EMBL; AB048423; BAB62712.1; -.

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Qy	654	KWELHQKRLLASTASSSSPASVWAKEDRN	684
Db	904	KWELHQKRLLASTASSSSPASVWAKEDRN	934
RESULT 5			
Qy	Q8VID6	PRELIMINARY;	PRT; 935 AA.
Id	Q8VID6		
AC	Q8VID6;		
DT	01-MAR-2002 (TrEMBLrel. 20, Created)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Phosphodiesterase 11A4..		
GN	RNPDE11A4.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		
OX	NCBI_TaxID=10116;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=21393948; PubMed=11502204;		
RX	RA Yuasa K., Ohguru T., Asahina M., Omori K.;		
RA	"Identification of rat cyclic nucleotide phosphodiesterase 11A		
RT	(PDE11A); comparison of rat and human PDE11A splicing variants.";		
RT	Eur. J. Biochem. 268:4440-4448(2001).		
RL	EMBL; AB059362; BAB79629.1; -		
DR	InterPro; IPR003018; GAF.		
DR	InterPro; IPR003607; ME_Ppase_Hdc.		
DR	InterPro; IPR002073; PDEase.		
DR	Pfam; PF01590; GAF; 2.		
DR	Pfam; PF002333; PDEase; 1.		
DR	PRINTS; PR00387; PDIESTERASE1.		
DR	SMART; SM00065; GAF; 2.		
DR	SMART; SM00471; HDC; 1.		
DR	PROSITE; PS00126; PDEASE_I; UNKNOWN_1		
DR	SEQUENCE 935 AA; 104570 MW; E80FE1039770P8276 CRC64;		
Qy	54	KDRRFNDEIDKLTGYKTKSLCCMPIRSSDGEIIGVQAQINKIPEGAPFTTEDDEKVNQMVL	
Db	304	QDRRFNDEIDKLTGYKTKSLCCMPIRNSDGEIIGVQAQINKIPEGPAPFTTEDDEKVNQMVL	
Qy	114	PCFGIAISNAQLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKKIMHRAOTLLKCRG	
Db	364	PCFGIAISNAQLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKKIMHRAOTLLKCRG	
Qy	174	SVLLLEDIESPVVKFTKSPELMSPKCSADAENSFKESMEKSSYSDWLINNSTAEIIVASTG	
Db	424	SVLLLEDIESPVVKFTKSPELMSPKCSADAENSFKESVEKSSYSDWLINNSTAEIIVASTG	
Qy	234	LPVNISDAYQDRPFEADAEQISGFHRSVLCVPIWNNSHQIITGVQAQVLRLODKGPFDDAD	
Db	484	LPVNISDAYQDRPFEADAEQISGFHRSVLCVPIWNNSHQIITGVQAQVLRLODKGPFDDAD	
Qy	294	QRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSTHATCSKAEDVKFAANIPLV	
Db	544	QRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSTHATCSKAEDVKFAANIPLV	
Qy	354	SELAIDDIHFDDFSLDVDAMITAAALRMFMEIWMQVKFKIDYETLCRWLLTVRKNTRMVLY	
Db	604	SELAIDDIHFDDFSLDVDAMITAAALRMFMEIWMQVKFKIDYETLCRWLLTVRKNTRMVLY	
Qy	414	HNWRHAFNVQCLMFAMLTAGFDQDILTEVEILAVIVGCLCHDLDRHGTNNAFOAKSGSAL	
Db	664	HNWRHAFNVQCLMFAMLTAGFDQDILTEVEILAVIVGCLCHDLDRHGTNNAFOAKSGSAL	
Qy	474	AQLYGTSAATLEHHHFNHAWILOSSEGHNTFAMLSKEYSDMLMQLKQSLATDLTLFYFR	
Db	724	AQLYGTSAATLEHHHFNHAWILOSSEGHNTFAMLSKEYSDMLMQLKQSLATDLTLFYFR	

Db 244 ANIPLVSELAIDDIHFDDFSLDVLDAITAAALRMFMELGMWQKFKIDYETLCRWLLTVRKN 303
 QY 408 YRMVLYHNHRHAFNVQMLFAMLTAGFQDILTEVEILAVIGCLCHDHRGTNNAFQA 467
 |||||
 Db 304 YRMVLYHNHRHAFNVQMLFAMLTAGFQDILTEVEILAVIGCLCHDHRGTNNAFQA 363
 |||||
 QY 468 KGSALAOLYGTSTATLEHHHFNHVMILQSGHNIFANLSSKEYSDLMQLLKQSLATDL 527
 |||||
 Db 364 KDSALAOLYGTSTATLEHHHFNHVMILQSGHNIFANLSSKEYSDLMQLLKQSLATDL 423
 |||||
 QY 528 TLYFERRTEFFELYSKGEYDHNKHNHRDIFRSLMTACDLGAVTKPWEISQVAELVTSE 587
 |||||
 Db 424 TLYFERRTEFFELYSKGEYDHNKHNHRDIFRSLMTACDLGAVTKPWEISQVAELVTSE 483
 |||||
 QY 588 FFEQDRERLEKLTPTSAIFDRNRKDELPRQLQLEWIDSICMPLYQALVKVNVKLPMLDS 647
 |||||
 Db 484 FFEQDRERLEKLTPTSAIFDRNRKDELPRQLQLEWIDSICMPLYQALVKVNVKLPMLDS 543
 |||||
 QY 648 VATNRKWEELHQRKLLASTA-----SSSSPASVMVAKEDR 683
 |||||
 Db 544 VAANRRKWEELHQRKLLASTA-----SSSSPASVMVAKEDR 580
 |||||

RESULT 8

Q9NY45
 ID Q9NY45 PRELIMINARY: PRT: 490 AA.
 AC Q9NY45
 DT 01-OCT-2000 (TremBLrel. 15, Created)
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Cyclic nucleotide phosphodiesterase 11A1.
 GN PDE11A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKETAL MUSCLE;
 RX MEDLINE=20202699; PubMed=10725373;
 RA Fawcett L., Baxendale R., Stacey P., McGrouther C., Harrow I.,
 Soderling S., Hewman J., Beavo J.A., Phillips S.C.;
 RT "Molecular cloning and characterization of a distinct human
 phosphodiesterase gene family:PDE11A.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:3702-3707(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20570133; PubMed=11121118;
 RA Yuasa K., Kanoh Y., Okumura K., Omori K.;
 RT "Genomic organization of the human phosphodiesterase PDE11A gene:
 Evolutionary relatedness with other PDEs containing GAF domains.";
 RL Eur. J. Biochem. 268:168-178(2001).
 DR EMBL: AJ251509; CAB82573.1; .
 DR EMBL: AB048423; BAB62714.1; .
 DR EMBL: AB048408; BAB62714.1; JOINED.
 DR EMBL: AB048409; BAB62714.1; JOINED.
 DR EMBL: AB048410; BAB62714.1; JOINED.
 DR EMBL: AB048411; BAB62714.1; JOINED.
 DR EMBL: AB048412; BAB62714.1; JOINED.
 DR EMBL: AB048413; BAB62714.1; JOINED.
 DR EMBL: AB048414; BAB62714.1; JOINED.
 DR EMBL: AB048415; BAB62714.1; JOINED.
 DR EMBL: AB048416; BAB62714.1; JOINED.
 DR EMBL: AB048417; BAB62714.1; JOINED.
 DR EMBL: AB048418; BAB62714.1; JOINED.
 DR EMBL: AB048419; BAB62714.1; JOINED.
 DR EMBL: AB048420; BAB62714.1; JOINED.
 DR EMBL: AB048421; BAB62714.1; JOINED.
 DR EMBL: AB048422; BAB62714.1; JOINED.
 DR InterPro: IPR003018; GAF.
 DR InterPro: IPR003607; ME_Pplase_Hdc.
 DR InterPro: IPR002073; PDEase.
 DR Pfam: PF01590; GAF; 1.

DR Pfam: PF00233; PDEase; 1.
 DR PRINTS; PR00387; PDISTERASE1.
 DR SMART; SM0065; GAF; 1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_1; 1.
 SQ SEQUENCE 490 AA; 55786 MW; 28FD77BC040834F4 CRC64;
 Query Match 72.3%; Score 2541; DB 4; Length 490;
 Best Local Similarity 100.0%; Pred. No. 8.1e-181;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 195 MSPKCSADAENSPKESMEKSSYSDWLNINNSTAEVLASTGLPVNLSDAYQDPRFADADQI 254
 |||||
 Db 1 MSPKCSADAENSPKESMEKSSYSDWLNINNSTAEVLASTGLPVNLSDAYQDPRFADADQI 60
 |||||
 QY 255 SGFHRSVLCVPIWNSNHQIIGVAQVNLNRDLGKFPDDADQRLFEAFVFCGLGINTTIMY 314
 |||||
 Db 61 SGFHRSVLCVPIWNSNHQIIGVAQVNLNRDLGKFPDDADQRLFEAFVFCGLGINTTIMY 120
 |||||
 QY 315 DQVKSWAKOSVALDVLISYHATCSKAEDKFKAAANIPLVSELAIDDIHFDDFSLDVLDAI 374
 |||||
 Db 121 DQVKSWAKOSVALDVLISYHATCSKAEDKFKAAANIPLVSELAIDDIHFDDFSLDVLDAI 180
 |||||
 QY 375 TAALRMFMELGMWQKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQMLFAMLTAG 434
 |||||
 Db 181 TAALRMFMELGMWQKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQMLFAMLTAG 240
 |||||
 QY 435 FQDILTEVEILAVIGCLCHDHRGTNNAFQAQSGSALAOLYGTSTATLEHHHFNHVM 494
 |||||
 Db 241 FQDILTEVEILAVIGCLCHDHRGTNNAFQAQSGSALAOLYGTSTATLEHHHFNHVM 300
 |||||
 QY 495 LQSEGHNIFANLSSKEYSDLMQLLKQSLATDLTYFERRTEFFELYSKGEYDWNKHNHR 554
 |||||
 Db 301 LQSEGHNIFANLSSKEYSDLMQLLKQSLATDLTYFERRTEFFELYSKGEYDWNKHNHR 360
 |||||
 QY 555 DIFRSMMLTACDLGAVTKPWEISQVAELVTSEFFEQDRERLEKLTPTSAIFDRNRKDE 614
 |||||
 Db 361 DIFRSMMLTACDLGAVTKPWEISQVAELVTSEFFEQDRERLEKLTPTSAIFDRNRKDE 420
 |||||
 QY 615 LPRLQLEWIDSICMPLYQALVKVNVKLPMLDSVATNRSKWEELHQRKLLASTASSSPA 674
 |||||
 Db 421 LPRLQLEWIDSICMPLYQALVKVNVKLPMLDSVATNRSKWEELHQRKLLASTASSSPA 480
 |||||
 QY 675 SVMVAKEDRN 684
 |||||
 Db 481 SVMVAKEDRN 490
 |||||

RESULT 9

Q9VJ79
 ID Q9VJ79 PRELIMINARY: PRT: 1284 AA.
 AC Q9VJ79
 DT 01-MAY-2000 (TremBLrel. 13, Created)
 DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE CG10231 protein.
 GN CG10231.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazewicz R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cusaw S.A., Dahle C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ihegwam C.,
RA	Jabali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reiner K.C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaverji J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT	"The genome sequence of <i>Drosophila melanogaster</i> ";
RL	Science 287:2185-2195(2000).
RL	EMBL; AF003659; AAF3675.1; -
DR	FlyBase; FBgn0032686; CG10231.
DR	InterPro; IPRO03018; GAF.
DR	InterPro; IPRO03607; ME_Plpase_HDC.
DR	InterPro; IPRO02073; PDEase.
DR	Pfam; PF01590; GAF; 2.
DR	Pfam; PF00233; PDEase; 1.
DR	PRINTS; PR00387; PDIESTERASE1.
DR	SMART; SM00065; GAF; 2.
DR	SMART; SM00471; Hdci; 1.
DR	PROSITE; PS00126; PDEASE_I; 1.
SR	SEQUENCE 1284 AA: 141726 MW: F6873C90A9953430 CRC64;
QY	Query Match 43.4%; Score 1511.5; DB 5; Length 1284;
QY	Best Local Similarity 44.0%; Pred. No. 1.4e-103;
QY	Matches 303; Conservative 126; Mismatches 202; Indels 51; Gaps 6
Db	20 KKVKTRLVQLTSGASLAEKQBKHQDFLIQRQT-----KTDDRPNDFI 62
Db	263 KCLLVSKFLDVCPRSTVEEMEQQBDEVAVAMGTAGHVABSGPVNIPDAYQDFENCI 322
QY	63 DKLTGYKTKSLLCMPIRSSDGEIGTGAQAINKPIPEGAPTTEDDEKYMWYLFPFCGTAISN 122
Db	323 DSLSYGRTKALLCMPIDKSSGDVITGAQVLINM-NGECSEIDEKFVSYYLFCFGIGLEN 381
QY	123 AOLFAASRKKEYRSALREVVNDLFQEOTLEKIVKKIMHRAOTLLKRCSCVLLLEDTE 182
Db	382 AOLYEKSQLEIKRNOVLDLARMIPEQSSTIEHWVFILTHMQSLIQCORVOLLVHEAD 441
QY	183 SPVVKFTKSFELMSPKCSADAENSFKESMEKSSYDWLINNSTAEILVASTGLPVNISTAY 242
Db	442 KG-SFSRVDFEANDLSEEEATSRTSPYE----SRPPINIGITHVAATTGETVNVPNAY 495
QY	243 QDPREDAAQDISGFHRISVLCVPWNNSHQITGVAQVLNRLDGKFPDDADQRLFAFVI 302
Db	496 EDORFDASVDENSCFKHSIIICMAIKNSLGQIIGVLIQINKFNELDFTKNDEFVFEAFI 555
QY	303 FCGLGINNTIMYDOVKKSWAKQVALDVLYSHATCSKAEDKE----- 345
Db	556 FCGMGILNHHTYETKAIRAIVMAKQSVTLVLSYHASATMDAEHRUKOKQOQAVGLRQAPL 615
QY	346 -----KAANIPLVSELAIIDDHFDDPSLDVDAMITAAIRMFWMELGMVKFK IDYET 396

Db	616	SLPRKKLQRLRLRVP	SAVHFRLHDFKEDDTHFEDDDTLKACLRMFLDLDVFERPHIDYEV	675
Qy	397	LCRWLLTVRKNYRWLV	YHNHRHAFNVCLMFAMLLTTAGFQDILTEVEILAVTGVCLCHDL	456
Db	676	LCRWLLSVKKNYRNVT	YHNHRHAFNVAGMFAILLTTQWKKIFGEICLALIIGLCHDL	735
Qy	457	DHRTGNNAQKSGSALA	QAQYGTSTATLEHHHNFHIAVMTLQSEGHNFANLSKSEYSDLMQ	516
Db	736	DHRTGNNSFQIKASSP	LAQLYSTS-TWBEHHFQCLMILNSPGNOILANLSSDDYCYRVR	794
Qy	517	LLKOSIILADLTLYFE	RTEFEFLVSKGEYDWNINKNHRDIFERSMLMTACDLCGAVTKPWEI	576
Db	795	VLEDAILLSTDLAVY	FKRGGPLESVQSTSWVAEPEPRALLURAMSMVTCDSLAIKTPWEI	854
Qy	577	SQVVAELVTSEFFQGR	DRERLELKTSPATIDRNRKDELPRQLQLEWIDSICMPLYOALVK	636
Db	855	EKRVAIDLVSSEFFQ	GDMEKQELNPTIDINRKEDELPMQVNFIDSLCLPIEAFAT	914
Qy	637	VNVKCLKPMLDSVAT	NRSKWEEL	658
Db	915	LSDKLEPLVEGVRD	NRGHIDL	936
RESULT 10				
Q95TW8	ID	Q95TW8	PRELIMINARY; PRT; 1018 AA.	
AC	095TW8;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	GH27433p.			
GN	CG8279.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BERKELEY;			
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,			
RA	Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,			
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,			
RA	Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,			
RA	Yu C., Lewis S.E., Rubin G.M., Celisner S.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY058470; AAL13699.1; .			
DR	FlyBase; FBgn0038237; CG8279.			
DR	InterPro; IPR003018; GAF.			
DR	InterPro; IPR002073; PDEase.			
DR	InterPro; IPR001230; Prenyl_site.			
DR	Pfam; PF01590; GAF; 2.			
DR	Pfam; PF00233; PDEase; 1.			
DR	PROSITE; PS00126; PDEASE_I; UNKNOWN_1.			
DR	PROSITE; PS00294; PRENYLATION; UNKNOWN_1.			
SO	SEQUENCE 1018 AA; 114668 MW; 8C758A607855EDD9 CRC64;			
Query Match 42.0%; Score 1478; DB 5; Length 1018;				
Best Local Similarity 45.7%; Pred. No. 3.le-101;				
Matches 305; Conservative 106; Mismatches 208; Indels 48; Caps				
Qy	28	VQISGASLAEKQKHODFL	IQRQTKDRRNDKLTGYKTKSLCMLCPRSSDGEIIG	87
Db	213	IGIAGMVAQTKQ-----	MIIMKAYKQARNCEIDLKTYKTNALCMPCINCEGDIIG	266
Qy	88	VAQAINKIPEGAPTEDE	KVQMYLPFCGGIAISNAQLFAASRKVEYRSRALLEVNDLF	147
Db	267	VAQIINKTNGCMEDEHD	VEIFRRLYTCGGIGQAQLFEMSQVEYRNRQIILLNARSIF	326
Qy	148	EEQTDLEKIVKIMHRAQ	TLKLCERCSSLLE-----DIESP-----VVKFTK	190
Db	327	EEONNLECLVTKITEAR	ELLKLCERCSSVELVDLDCCEASHLEKILEKPNOPATRAIKSAD	386


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Db 792 ILY-TTSMHEHFDHFLAAFLDRLAARRALRDALRELLDLVELVVDPTLIELVIEY 850
QY 491 -----AVMLIQS----- 497
Db 851 FLLRLRTFLPELDEDDDDVSDVSVVSVLVLDLVLVLSAALTWATYKTTIER 910
QY 498 -----EGHNIFANLSSKEYSDLMQLLKOSILATDLTYFFERTTEFFELYSKGEYDWNKIH 553
Db 911 TKTRDRNEMLDALSPEDYRSVMKTVESAILSTDLAMYFKKRNAPFLVELVEGEFDQGEK 970
QY 554 RDRFSMLMTACDLGAVTKPWEISROVAELVTSFEFGDRRLRLKLTTPSAIFDRNRKD 613
Db 971 KDLICGMNMTACDVAIAKPEVQHVAKLVADFEFDQGLKQLNTQPVAMMDRERKD 1030
QY 614 ELPRLOLEWIDICPMQYQALVKNVVKLPMDSVATNRKWEELHOK 661
Db 1031 ELPMQVGFIDVICLPLRVLCDTFPWITPLYEGTLENRRNQDLAEK 1078

RESULT 12
Q912Q1
ID Q912Q1 PRELIMINARY; PRT; 861 AA.
AC Q912Q1
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CGMP phosphodiesterase 6c.
GN PDE6C
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=RETINA;
RA Chang B., Hawes N.L., Hurd R.E., Davisson M.T., Nusinowitz S.,
RT Heckenlively J.R.;
RT "A sequence alteration in pde6c gene causes cone photoreceptor
RT function loss (cpfl1) in mice.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411063; AAK96254.1; -.
DR MGD; MGI:105936; Pde6c.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PROSITE; PS00126; PDEASE_1; UNKNOWN_1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 861 AA; 98785 MW; C582D78114652B5B CRC64;

Query Match 30.0%; Score 1054.5; DB 11; Length 861;
Best Local Similarity 35.5%; Pred. No. 8.1e-70;
Matches 243; Conservative 130; Mismatches 242; Indels 69; Gaps 16;

QY 54 KORFENDEIDKTYKTKSLCMLPSSDGEIIGVAQAINKIPEGAP-FTEDEKVMQY 112
Db 160 KNSHESDFMDKQGTGYTRNLLAVPIVAGK-EVLAVVMVANKI--SAPEFSKODEEVSFY 216
QY 113 LPFCGIAISNAQLFAASRKEYERSRALLLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCR 172
Db 217 LSFVAVALRQHTSVLYSVESRRSQILMMSANKVFEEITDVERQHKALYTIIRTINLNR 276
QY 173 CSVLLI-----EDIESPVVKTKSFELMSPKCSADAENSF-----KESWE--KS 214
Db 277 YSIGLLDWTKEFEYDEWPKLGEVEPKPTPDGRIIFYKIIDIYLHGKEEINVPIS 336
QY 215 SYSD-WLINNSTAELVASTGLPVNTSDYQDPDFDAEADQI--SGFHRSVLCVPTWNSN 271
Db 337 PRADHWTLVSGLPTVAENGFTCNMLNAPADEYFFQKGPVDYETGWIKNVLSLPLVKK 396
QY 272 HQIIGVAQVNLRLDGLKPFDDADQRLFEAFVIFCGLGINNNTIMYDQVKKSWAKQSVLDVL 331
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Db 397 EDIVGVATFYNRKDGKPFDEHDEHITETLTQGLWSLLNTDTYERNVKLESRKDIAQEMV 456
QY 332 SVHATCSRAEVD---KFK-AAANIPLVSE-----LAI-----DDIH---FDDFSL 368
Db 457 MNLTKATPDEISSILKFEKLNVEIECEERQLLAILKEDLPDPTADLYEFCSDPPI 516
QY 369 DVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNNRHAFNVQLMFA 428
Db 517 TEHELVKCGLRLFLFINVVEKFKVPVEVLTRWMTYVRKGYRPTVYHNNRHGFNVGQMTFT 576
QY 429 MTTTAGFQDILTEVEILAVIVGCLCHDHDHRTGNNAFQAKSGSALAQLYGTSATLEHHIF 488
Db 577 LLMTGRLKKYITDLEAFAMLAFAFCHDIDHRTNNTLYOMKSTSPLARLHGT--ILERHHL 635
QY 489 NHAIVMLQSEGHNIFANLSSKEYSDLMQLLKOSILATDLTYFFERTTEFFELYSKGE--- 545
Db 636 EYSKILLQDESINIFONLNKROFETVILHFEVATITADLYFKKRTMFKQIVDTCBQM 695
QY 546 -----YDWNINKHRDIFRSMLTACDILGAVTKPWEISROVAELVTSFEFGDRERLE 598
Db 696 SEETIKYVTSPTKKEVIMAMMTACDLSAITKPWEVQSQVALLVANEFEQDGLERTV 755
QY 599 LKLTSAITPDRNKDELPRQLLEWIDISCMPLYQALVKNVVKLPMDSVATNRKWEEL 658
Db 756 LQQQPTPMMDRSKDELKPLQVGFIDFVCTFYVKEFSRPHGEITPMLNGLQNNRVEWKS 815
QY 659 HOKRLLASTASSSSPASVMVAKED 682
Db 816 -----AEEYEAKVKVTBEE 829

RESULT 13
Q8UUY6
ID Q8UUY6 PRELIMINARY; PRT; 857 AA.
AC Q8UUY6;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Retinal PDE6 beta subunit.
GN PDE6B.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Li N., Baehr W.;
RT "Frog retina PDE6 subunits.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY044175; AAK95400.1; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; MEL_pplase_Hdc.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_1; UNKNOWN_1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 857 AA; 99213 MW; 562B8549E5B650E8 CRC64;

Query Match 29.0%; Score 1021; DB 13; Length 857;
Best Local Similarity 33.8%; Pred. No. 2.5e-67;
Matches 228; Conservative 131; Mismatches 250; Indels 66; Gaps 11;

QY 42 HODELQRTKTKDRFRNDEIDKTYKTKSLCMLPSSDGEIIGVAQAINKIPEGAP 101
Db 145 HTKKTINKDVSDETTYSRFADLEYKTKNLIAITPIMNGK--DVVAIVAMVWK--TDGSTF 202
QY 102 TEDDEKVMOMYLPFCGIAISNAQLFAASRKEYERSRALLLEVNDLFEEQTDLEKIVKIM 161
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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	1366.5	38.9	875	1	JW0106	3', 5'-cyclic-GMP p	
2	1355.5	38.6	875	1	A48719	3', 5'-cyclic-GMP p	
3	1050	30.1	862	2	I50186	3', 5'-cyclic-GMP p	
4	1047	29.8	859	2	B34611	3', 5'-cyclic-GMP p	
5	1039.5	29.6	855	2	A34810	3', 5'-cyclic-GMP p	
6	1037.5	29.5	858	2	JC4520	3', 5'-cyclic-GMP p	
7	1030	29.3	859	2	SI3030	3', 5'-cyclic-GMP p	
8	1027	29.2	856	1	A47451	3', 5'-cyclic-GMP p	
9	1026	29.2	859	1	S06418	3', 5'-cyclic-GMP p	
10	1025	29.2	856	2	S30762	3', 5'-cyclic-GMP p	
11	1020	29.0	854	2	A42828	3', 5'-cyclic-GMP p	
12	1009	28.7	853	2	A36617	3', 5'-cyclic-GMP p	
13	976	27.8	800	2	SI3032	3', 5'-cyclic-GMP p	
14	933.5	26.6	928	1	JC2486	3', 5'-cyclic-nucle	
15	920.5	26.2	921	1	A40981	3', 5'-cyclic-nucle	
16	920	22.5	393	2	S25590	hypothetical prote	
17	535.5	15.2	841	1	S24462	probable 3', 5'-cyc	
18	535.5	15.2	918	2	D88544	protein R08D7.6 [i	
19	381	10.8	536	2	I67945	3', 5'-cyclic-nucle	
20	365	10.4	712	2	S71626	3', 5'-cyclic-nucle	
21	364	10.4	673	2	I61358	3', 5'-cyclic-nucle	
22	362.5	10.3	610	2	I67946	3', 5'-cyclic-nucle	
23	362.5	10.3	844	2	I53865	phosphodiesterase	
24	362.5	10.3	886	2	A54442	3', 5'-cyclic-nucle	
25	362	10.3	584	2	B53109	3', 5'-cyclic-nucle	
26	362	10.3	672	2	I61259	3', 5'-cyclic-nucle	
27	357.5	10.2	859	2	AC2089	adenylate cyclase	
28	350	10.0	535	1	A46378	3', 5'-cyclic-nucle	
29	350	10.0	535	1	A44161	3', 5'-cyclic-nucle	

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Db 584 LVQNFOMKHEVLCRWILSVKKNYRNKRNVAHNNRHAFTNAQCMFAAKGAKGKIQNKLTDLIEI 643
Qy 445 LAVIVGCLCHDLDRGTNNNAQKSGSALAOLYGTSTATLEHHHFNHVAHMILOQSEGNIFA 504
Db 644 LALLIAALSHDLDRGVNNSYQIORSHPALQY-CHSTMEHHFDOCLMILNSPQNQLS 702
Qy 505 NLSKEYSDLMOLKQSLATDLTLTYFERRTEFFELVSKGEYDWNKKNRDIIFRSLMLTA 564
Db 703 GLSIEYKTKLIKQAILATDLALYIKRRGEFFELIRKNQFNLDHPQKELFLAMLMTA 762
Qy 565 CDLGAVTKPWEISROVAELVTSEFPEQDGRERLEKLTPTSAIFDRNRKDELPRLOLEWID 624
Db 763 CDLSAITKWPQIQRIAELVATEFFDQGRERLEKLTPTSAIFDRNRKDELPRLOLEWID 822
Qy 625 SICMPLYQALVKVNVKPKMLDSVATNRSKWEEEL--HOKRLLASTASSSS 672
Db 823 AICLQLYEALTHVSEDCFPDLDGCRKNKQKQWALAEQOEKMLINGESQQA 872

RESULT 2
A48719
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - bovine
N:Alternate names: PDE5A1
C:Species: Bos primigenius taurus (cattle)
C:Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 26-Aug-1999
C:Accession: A48719; A35807
R:McAllister-Lucas, L.M.; Sonnenburg, W.K.; Kadlecsek, A.; Seger, D.; Le Trong, H.; Colbran, R.J. Biol. Chem. 268, 22863-22873, 1993
A:Title: The structure of a bovine lung cGMP-binding, cGMP-specific phosphodiesterase de
A:Reference number: A48719; MUID:94043054; PMID:8226796
A:Accession: A48719
A:Molecule type: mRNA
A:Residues: 1-875 <MCA>
A:Cross-references: GB:L16545
A:Experimental source: lung
A:R:Thomas, M.K.; Francis, S.H.; Corbin, J.D.
J. Biol. Chem. 265, 14971-14978, 1990
A:Title: Substrate- and kinase-directed regulation of phosphorylation of a cGMP-binding
A:Reference number: A35807; MUID:90368672; PMID:2168396
A:Accession: A35807
A:Molecule type: protein
A:Residues: 90-101 <THO>
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A; 3',5'-cyclic-nucleotide phosphodie
C:Keywords: alternative splicing; cGMP binding; phosphoprotein; phosphoric diester hydrol
F:602-825/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F:92/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predicted

Query Match 38.6%; Score 1355.5; DB 1; Length 875;
Best Local Similarity 42.9%; Pred. No. 3.7e-84;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;

Qy 54 KDRFNDEIDKLTGYKTKSLICMPTRSSDGEIIGVAQAIN-KIPEGAPFTEDEKVMQY 112
Db 237 EDPNFAEDVQITGYKTSILICMPTRSSDGEIIGVAQAIN-KIPEGAPFTEDEKVMQY 112
Qy 113 LPFCGIATSNALQFAASKEYRSRALLLEVYNDLFEEQTDLEKIVKTMHRAQTLKACER 172
Db 297 LAFCGIVLHNAQLVETSLLENKRNQVLDLALIFEEOQSLEVLKIAATNIIISPMQVK 356
Qy 173 CSVLLEDIESPVVKFTKSFELMSPKCSADAENSF-----ESMEKSSYDML----- 220
Db 357 CTIFIVD-----DCSDSFSSVFHMECELEKS--SDTLTRERD 393
Qy 221 ---INNSTAEIVASTGLPVNISDAYQDPREDADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 394 ANRINWTAQVYKKNIMEPLNIPDVSKDKRFPWTNENMGNTNQCCIRSLCTPIKNGKKN 453
Qy 274 IIGVAQVNLRLDG-----KPEDDADQRLFEAFVIFCGILGINNTIYDQVKKSWAKQSV 328
Db 454 VIGVQVLVNMKEETTGKVKAFNRNDEQFLFEAFVIFCGILGIONTOYEAVERAKQVTL 513
Qy 329 DVLSYHATCSK---AEVDKPKAAINPLVSELAIDDIHFDDFSLDAMDAMITAAALRMFMELG 385
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Db 514 EVLSYHSAABEETRELQSLAAAVVPSAQTLLKIDTFSFSDFELSDELTALCTIRMFTDLN 573
Qy 386 MVQKFKIDYETLCRWLLTVRKNYR-VLYHNHRHAFNVCOLMFAMLTITAGQDILTEVEI 444
Db 574 LVQNFOMKHEVLCRWILSVKKNYRNKRNVAHNNRHAFTNAQCMFAAKGAKGKIQNKLTDLIEI 633
Qy 445 LAVIVGCLCHDLDRGTNNNAQKSGSALAOLYGTSTATLEHHHFNHVAHMILOQSEGNIFA 504
Db 634 LALLIAALSHDLDRGVNNSYQIORSHPALQY-CHSTMEHHFDOCLMILNSPQNQLS 692
Qy 505 NLSKEYSDLMOLKQSLATDLTLTYFERRTEFFELVSKGEYDWNKKNRDIIFRSLMLTA 564
Db 693 GLSIEYKTKLIKQAILATDLALYIKRRGEFFELIRKNQFNLDHPQKELFLAMLMTA 752
Qy 565 CDLGAVTKPWEISROVAELVTSEFPEQDGRERLEKLTPTSAIFDRNRKDELPRLOLEWID 624
Db 753 CDLSAITKWPQIQRIAELVATEFFDQGRERLEKLTPTSAIFDRNRKDELPRLOLEWID 812
Qy 625 SICMPLYQALVKVNVKPKMLDSVATNRSKWEEEL--HOKRLLASTASSSS 672
Db 813 AICLQLYEALTHVSEDCFPDLDGCRKNKQKQWALAEQOEKMLINGESSQT 862

RESULT 3
150186
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: 150186
R:Semple-Rowland, S.L.; Green, D.A.
Exp. Eye Res. 59, 365-372, 1994
A:Title: Molecular characterization of the alpha'-subunit of cone photoreceptor cGMP
A:Reference number: 150186; MUID:95121406; PMID:7821382
A:Accession: 150186
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-862 <SEM>
A:Cross-references: GB:L29233; NID:g495742; PIDN:AAC42223.1; PID:g495743
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 30.1%; Score 1060; DB 2; Length 862;
Best Local Similarity 32.8%; Pred. No. 4.6e-64;
Matches 233; Conservative 139; Mismatches 251; Indels 88; Gaps 12;

Qy 25 TRLVQISGASLAERKQKHQDFLIQRTK-----KDRFN 59
Db 112 TRLLNVTPTS-----KFDNLVNPDKETVPLDGIAGVVAHTKFFNIPDVKKNNHFS 165
Qy 60 DEIDKLTGYKTKSLICMPTRSSDGEIIGVAQAIN-KIPEGAPFTEDEKVMQYLPFCGIA 119
Db 166 DYLDKTKGYTTVNMMALPI-TQGREVLAVVWALNKL-NASEFSKEDEEVFKKYLNFSLV 223
Qy 120 ISNAQLFAASKEYRSRALLLEVYNDLFEEQTDLEKIVKTMHRAQTLKACERGVSLV- 178
Db 224 LRNHSTLYLVNIESRRSQMLLSANKVFEELTDIERQFHKALYTRMYLNCERYSGVGLD 283
Qy 179 -----EDIESPVVKFTKSFELMSPKCSADAENSF-----KESME---KSSYDML 220
Db 284 MTKKEFYDEWPIRLGEAEPYKGPKTPDGRVENVFKIIDIILHGKEETKIVTPPADHWC 343
Qy 221 INNSIAELVASTGLPVNISDAYQDPREDADQISGFH---IRSVLCVPIWNHIOITGA 278
Db 344 LISGLPTVYAENGFCNMNAPADEYTFQKGPVDETGWIKNVLSLPIVKNKEIVGVA 403
Qy 279 QVNLRLDKGPFDDAQRLFEAFVIFCGILGINNTIYDQVKKSWAKQSVLDSYHATCS 338
Db 404 TFYNRKDGKPFDEYDEQIETLTQFLGNSVLNTDTYDKMKNLENKRDIAQELMYQTKAT 463
Qy 339 KAQVD---KPK-----AANPLVSELAIDDIHFDDFSLDAMDAMIT 375
```

Db 464 PTEVESILKYKEKUNVKSIECDKDLIRILKEELPKDKLELYEFRRSDFPVTEHGLIT 523
Qy 376 AALRMFMELGVMQVKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVCOLMFTAGF 435
Db 524 CGIRLFEINVEKFKPAEVLTRWYTVRGYRDITYHNHRHGFNVGQTFILMTGRI 583
Qy 436 QDILTEVEILAVIVGCCILCHDLDRGTNNAFQAKSGSALAQLYGTSALEHHFHVAMIL 495
Db 584 KKYVTDLEAFAMVAAAFCHDIDHRGTNNLYQMSAAPLAKLHG-SSILERHLEYSKTL 642
Qy 496 QSEGHNFANLSKEYSDLMOLLKQSILATDLTLYFERRTEFFELVSKGE----- 545
Db 643 QDESILFONLKQFETVHLFEVATIDTDLALYFKKRTMFQKIVDAIERKMETEPAIK 702
Qy 546 YDNWIKNHRDIFRSMILMTACDLGAVTKPWEISROVAELVTSEFFEQDGRLEKLTPSA 605
Db 703 YISIDPTKKEVIMAMMTGCDLSAITKPEVQSVKALVANEFWEQDGLERTVLOQOPIP 762
Qy 606 IFDRNRKDELPRLOLEWIDSCMPLYQALVKVNVKLPMLDSVATNRSKWE 656
Db 763 MMDNRKGDLPKLVQGFDFVCTFVYKEFSRFHKEITPMFDGLQNNRVEWK 813

RESULT 4
B34611
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 21-Jan-2000
C:Accession: B34611
R:Pittler, S.J.; Baehr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen,
Genomics 6, 272-283, 1990
A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi-
esterase
A:Reference number: A34611; MUID:90165986; PMID:2155175
A:Accession: B34611
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-859 <PI>
A:Cross-references: GB:M26061
C:Genetics:
A:Gene: GDB:PDE6A; PDEA
A:Cross-references: GDB:120265; OMIM:180071
A:Map position: 5q31.2-5q34
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 29.8%; Score 1047; DB 2; Length 859;
Best Local Similarity 33.1%; Pred. No. 3.5e-63;
Matches 229; Conservative 136; Mismatches 246; Indels 80; Gaps 12;

Qy 54 KDRFNDEIDKLTGYTKSLCMLPIRSSDGEIIGVAQAINKIPGAPTEDEKVMQMYL 113
Db 158 EDEHCFDVLITTEYKTNILASIPMGK-DVVAIMAVNKV-DGSHFTKDEILLKYL 215
Qy 114 PFCGIATISNAOLFAASKEYERSRALLEVNDLFEEDTLEKIYKIMHRAQTLLKCERC 173
Db 216 NFANLIMKWHLSYLHNCETRRGQILLWSGSKVFEELTDIERQFHKALYTVRAFLNCDRY 275
Qy 174 SVLLLEDIESPVVFTKSFEL-----MSPKCSADAENSF-----KESME 212
Db 276 SVGLLD-----MTQKEEFDVWVLMGEVPPYSGPRTPDGGINEFYKVIDYILHGKEDIK 330
Qy 213 ---KSSYSDWLINNSIAELVASTGLVPVNISDAYODPRDAEADQI--SGFHRSVLCVPI 267
Db 331 VIPNPPDHVALVSLPTYYAONGLICINMAPSEDFAFQKEPLDESGWIKWLSNPI 390
Qy 268 WNSNHQITGVAQVNLNLDGKPFDDADQRLFAFVIFCGLGINTIMYDOVKKSWAKQSV 327
Db 391 VNKKEEIVGATFYNRKDGKPFDEMDETLMESLTQFLGWSVLPDPTESMKNLENRKDIF 450
Qy 328 LDVLSYHATCSKAEDK-----FKAANIPLVSELAIDDIHFD 365
Db 451 QDVIKHYVKDNEEIQRLTKTREYVYKPEWCEBEEELAEILLOAELPDADKYEINKFHFSD 510

Qy 366 FSLDWDAMITAAALRMFMELGVMQVKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVCOL 425
Db 511 LPLTELELVKCGIQMYVELKVDKFIHQEALVRFMYSLSGYRKITYHNHRHGFNVGQT 570
Qy 426 MFAMLTITAGFODIITEVEILAVIVGCCILCHDLDRGTNNAFQAKSGSALAQLYGTSALEH 485
Db 571 MFSLLVTGCKLRKYPTDLEAFAMVAAAFCHDIDHRGTNNLYQMSAAPLAKLHG-SSILER 629
Qy 486 HHFNHAVNIIQSEGHNFANLSKEYSDLMOLLKQSILATDLTLYFERRTEFFELVSKGE----- 542
Db 630 HHLEFGTKLLRDESLNIFONLRROHHAHIMMDIAIATDIALYFKKRTMFQKIVDOQSK 689
Qy 543 --KGEYDWN-----IKNHRDIFRSMILMTACDLGAVTKPWEISROVAELVTSEFFEQDGR 595
Db 690 TYESEQEWQYMLLEQTKRKIEVMAMMTACDLSAITKPEVQSVQVALLVAAEFWEQDGL 749
Qy 596 RLEKLTPSAIFDRNRKDELPRLOLEWIDSCMPLYQALVKVNVKLPMLDSVATNRSKW 655
Db 750 RTVLQONPIPMDNRKADLPKLVQGFDFVCTFVYKEFSRFHKEITPMFDGLITNNRKEW 809
Qy 656 -----EELHOKRLLASTASSSS 672
Db 810 KALADEYDAKMKVQEEKKQOOSAKSAAGN 840

RESULT 5
A34810
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha' chain, cone - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jan-2000
C:Accession: A34810; A34809
R:Li, T.; Volpp, K.; Applebury, M.L.
Proc. Natl. Acad. Sci. U.S.A. 87, 293-297, 1990
A:Title: Bovine cone photoreceptor cGMP phosphodiesterase structure deduced from a cD
A:Reference number: A34810; MUID:90115860; PMID:2153291
A:Accession: A34810
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-855
A:Cross-references: GB:M37838; NID:g163490; PIDN:AAA30687.1; PID:g163491; GB:M29465
R:Charbonneau, H.; Prusti, R.K.; Leffron, H.; Sonnenburg, W.K.; Mullaney, P.J.; Walsh
Proc. Natl. Acad. Sci. U.S.A. 87, 288-292, 1990
A:Title: Identification of a noncatalytic cGMP-binding domain conserved in both the c
A:Reference number: A34809; MUID:90115859; PMID:2153290
A:Accession: A34809
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-855
A:Cross-references: GB:M37838; NID:g163490; PIDN:AAA30688.1; PID:g163493; GB:M29465
A:Note: parts of this sequence were confirmed by protein sequencing
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 29.6%; Score 1039.5; DB 2; Length 855;
Best Local Similarity 35.5%; Pred. No. 1.1e-62;
Matches 234; Conservative 119; Mismatches 249; Indels 57; Gaps 11;

Qy 54 KDRFNDEIDKLTGYTKSLCMLPIRSSDGEIIGVAQAINKIPGAPTEDEKVMQMYL 113
Db 155 KNSHFSDFMDQGTGYVTRNLLATPIVMGK-EVLAVFMAVNVK-DASEFSKODEEVFSKYL 212
Qy 114 PFCGIATISNAOLFAASKEYERSRALLEVNDLFEEDTLEKIYKIMHRAQTLLKCERC 173
Db 213 SFVSIILKLHNTNYLNIESRRSQLMWSANKVFEELTDVERQHFHKLTVRTYLNCERY 272
Qy 174 SVLLLD-----EDIESPVVFTKSFELMSPKCSADAENSF-----KESME---KS 214
Db 273 SIGLLDWTKEKEFYDENPVLGEVPEYKPKTPDGRVIFIKYIDYILHGKEEIKVPTTP 332
Qy 215 SYSDWLINNSIAELVASTGLVPVNISDAYODPRDAEADQI--SGFHRSVLCVPIWNSNH 272

Db 333 PMDHWTLISGLTYVAENGFCINMMLNAPADEYFTQKGPVDETGWIKNVLSLPIVKNKE 392
QY 273 QIIGVAQVNLRLDGRPFDDADQORFEAFVIFCGLGINNNTIMYDQVKKSWAKOSVALDVLS 332
Db 393 DIVGVATYNNRKGDPFDEYDEHIAETLTQFLGWSLLNTDYKKNKLENKRDIAQEMLM 452
QY 333 YHATCSKAEDV---KFK-AANIPLVSELA-----IDDIHFDDFSLD 369
Db 453 NHTKATPDEIKSILKFEKLNIDVIEEDCEKQVLTILKEDLPDPTADLYEFPFRHLPI 512
QY 370 VDMITAAALRMFMELGMVQKIDYETLCRWLLTVRKNYRMVLYHNWRAFNVCOLMFAM 429
Db 513 EHELKGLRFFFEINVEKEKVPVEVLTVMYTVRKGIRAVTYHNHRHGFNVGOTMFTL 572
QY 430 LTTAGFQDILTVEILAVIVGCLCHDLHRGTNNAFQAKSGSALAQLYGTSTATLEHHFN 489
Db 573 LMTGLRKKYYTDLFAFAMLAFAFCHDIDHRTGNLNLYOMKSTSPARLHG-SSILERRHLE 631
QY 490 HAVMILOSEGHNIIFANLSKEYSDLMQLLKOSILATDLTYLFFERTFEFFELVSKGE---- 545
Db 632 YSKTLQDESINIFONLNKROVETVIHLFEVAIIATDLALYFKKRTMFKQIVDACEKMET 691
QY 546 -----YDWNKIKHNRDIFRSMLMTACDLGAVTKPWEISROVAELVTSFEFFQGDRLERLEL 599
Db 692 EEEAIKYVTIDTKKEIIMAMMTACDLSAITKPWEVQSVALLVANFEWEGQDLERTVL 751
QY 600 KLTPSAIFDRNKDELPRQLQLEWIDSICMPLYQALVKNVKLKPMLDSVATNRSKWEEL 658
Db 752 QOOPIPMMDRNKKDELPLQVCFIDFVCTFVYKFSRHFKEITPMLSLQNNRVKESL 810
RESULT 6
JC4520
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha' chain - human
C:Species: Homo sapiens (man)
C>Date: 08-Feb-1996 #sequence_revision 11-Apr-1997 #text_change 20-Jun-2000
C:Accession: S63688; JC4520
R:Reschenko, E.A.; Andreeva, S.G.; Suslova, V.A.; Smirnova, E.V.; Zagranichny, V.E.; Li
FEBS Lett. 381, 149-152, 1996
A:Title: Human cone-specific cGMP phosphodiesterase alpha' subunit: complete cDNA sequen
A:Reference number: S63688; MUID:96193933; PMID:8641425
A:Accession: S63688
A:Molecule type: mRNA
A:Residues: 1-858 <FES>
A:Cross-references: EMBL:X94354; NID:gl1616594; PIDN:CAA64079.1; PID:gl149517
A:Note: Intron positions were determined by partial sequencing of genomic DNA
R:Vicizian, A.S.; Piriev, N.I.; Farber, D.B.
Gene 166, 205-211, 1995
A:Title: Isolation and characterization of a cDNA encoding the alpha' subunit of human c
A:Reference number: JC4520; MUID:96125191; PMID:8543163
A:Accession: JC4520
A:Molecule type: mRNA
A:Residues: 1-115 'V', 117-269 'S', 271-372 'P', 374-463 'L', 465-564 'O', 566-858 <VIC>
A:Cross-references: GB:U31973; NID:g940230; PIDN:AA96392.1; PID:g940231
A:Note: this sequence lacks a residue Tyr after the 231-Met, and has an additional resid
C:Genetics:
A:Gene: alpha'-pde
A:Introns: 160/3; 211/3; 241/3; 288/3; 313/3; 335/2; 357/3; 373/3; 423/3; 471/3; 494/3;
A:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
C:Keywords: cGMP binding; lipoprotein; phosphoric diester hydrolase; photoreceptor; pren
F:560-770/Domain: catalytic #status predicted <CAT>
F:561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F:855/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 29.5%; Score 1037.5; DB 2; Length 858;
Best Local Similarity 35.1%; Pred. No. 1.5e-62;
Matches 231; Conservative 122; Mismatches 249; Indels 57; Gaps 11;

QY 54 KDRFNDEIDKLTGYKTKSLCMLPISRSDGEIIGVAQAINKIPGAPFTEDEKVMOMYL 113
Db 160 KNSHFSDFMDQGTGYTKNLLATPIVGVK-EVLAVIMAVNKV-NASESKODEEVFSKYL 217
QY 114 PFCGIATISNAQLFAASRKEYERSRALLEVNDLFEQTDLEKIVKIMHRAQTLLKCERC 173

Db 218 NFVSIILRLHHTSYMYNIESRRSOTILMMSANKVPELTVDVQPHKALYTVRTYLCNERY 277
QY 174 SVILL-----EDIESPVVKTKSELMSPKCSADAENSF-----KESME---KS 214
Db 278 SIGLLDMTKKEFYDEWPIKLGVEPYKGPRTDGRVNFYKIIDYILHGREIKVPTP 337
QY 215 SYSDWLNNISIAELVASTGLPNIISDAYODREFDAEADQI--SGPHIRSVLCVPTWNSNH 272
Db 338 PADHWTLISGLTYVAENGFCINMMLNAPADEYFTQKGPVDETGWIKNVLSLPIVKNKE 397
QY 273 QIIGVAQVNLRLDGRPFDDADQORFEAFVIFCGLGINNNTIMYDQVKKSWAKOSVALDVLS 332
Db 398 DIVGVATYNNRKGDPFDEYDEHIAETLTQFLGWSLLNTDYKKNKLENKRDIAQEMLM 457
QY 333 YHATCSKAEDV---KFK-AANIPLVSE-----LAIDDIHFDDFSLD 369
Db 458 NHTKATPDEIKSILKFEKLNIDVIEEDCEKQVLTILKEDLPDPTADLYEFPFRHLPI 517
QY 370 VDMITAAALRMFMELGMVQKIDYETLCRWLLTVRKNYRMVLYHNWRAFNVCOLMFAM 429
Db 518 EHLKGLKCGIRLFFFEINVEKEKVPVEVLTVMYTVRKGIRAVTYHNHRHGFNVGOTMFTL 577
QY 430 LTTAGFQDILTVEILAVIVGCLCHDLHRGTNNAFQAKSGSALAQLYGTSTATLEHHFN 489
Db 578 LMTGLRKKYYTDLFAFAMLAFAFCHDIDHRTGNLNLYOMKSTSPARLHG-SSILERRHLE 636
QY 490 HAVMILOSEGHNIIFANLSKEYSDLMQLLKOSILATDLTYLFFERTFEFFELVSKGE---- 545
Db 637 YSKTLQDESINIFONLNKROFETVIHLFEVAIIATDLALYFKKRTMFKQIVDACEQMT 696
QY 546 -----YDWNKIKHNRDIFRSMLMTACDLGAVTKPWEISROVAELVTSFEFFQGDRLERLEL 599
Db 697 EEEAIKYVTIDTKKEIIMAMMTACDLSAITKPWEVQSVALLVANFEWEGQDLERTVL 756
QY 600 KLTPSAIFDRNKDELPRQLQLEWIDSICMPLYQALVKNVKLKPMLDSVATNRSKWEEL 658
Db 757 QOOPIPMMDRNKRDELPLQVCFIDFVCTFVYKFSRHFKEITPMLSLQNNRVKESL 815
RESULT 7
SI3030
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI3030
R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase al
A:Reference number: SI3030; MUID:91130581; PMID:1847109
A:Accession: SI3030
A:Molecule type: DNA
A:Residues: 1-859 <BAE>
A:Cross-references: EMBL:X60664; NID:g53587; PIDN:CAA43072.1; PID:g53588
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
Query Match 29.3%; Score 1030; DB 2; Length 859;
Best Local Similarity 32.9%; Pred. No. 5e-62;
Matches 227; Conservative 133; Mismatches 251; Indels 80; Gaps 12;

QY 54 KDRFNDEIDKLTGYKTKSLCMLPISRSDGEIIGVAQAINKIPGAPFTEDEKVMOMYL 113
Db 158 EDEHCFDVLNLTGYTKNLLASPMNGK-DVAIIMAVNKID-PHETRDEEILLKYL 215
QY 114 PFCGIATISNAQLFAASRKEYERSRALLEVNDLFEQTDLEKIVKIMHRAQTLLKCERC 173
Db 216 NFVNLINKVPHLSVYLHNCEITRRGILLWSGSKVFEELTDIERQPHKALYTVRAFLNCDRY 275
QY 174 SVLLLEDIESPVVKTKSFEL-----MSPKCSADAENSF-----KESME 212

Db 276 SVGLLD-----MTKQKEFFDVPVLMGEAPAYSGPRTPDGRINFYKVIDYILHGKEDIK 330
 Qy 213 ---KSSYSDMLNINNSIAELVASTGLPNISDAYODPRFDAEADQI--SGFHRSVLCVPI 267
 Db 331 VIPNPPADHVALVSGLPYVAQNLGINIMNAPAEDEFQKPELDESQWIKNVLSMPI 390
 Qy 268 WNSHQLIIGVAQVNLRLDGKPFDDADQRLFEAFVIFGGLGNNTIMYDQVKKSWAKOSVA 327
 Db 391 VNKEEIVGVATFYNRKDGKPFDDMDLTLQFLGWSVLPNDTYESMKNLENRKDI 450
 Qy 328 LDVLSYHATCSKAEVDKFAA-----NIPVLSLAIDDIHFD 365
 Db 451 QDIVKYHVQKDNEDQILKTREVYKPEWCECEEEELAEILQRLPEAEYENKHFSD 510
 Qy 366 FSLDVSAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNRHAFNVCQL 425
 Db 511 LPLTELELVKCGIQMYELRWKDFHPIQOEALVRFYMSLSKGYRRIYHNRHGFNVGQT 570
 Qy 426 MFAMLTITAGFDQILTEVEILAVIVGCLDHRGTNNATQAKSGSLAQIYGTSALEH 485
 Db 571 MFSLLVTGKLRKRYPTDLEALAWTAAFCHDIDHRTNNLYQMKSONPLAKLHG--SSILER 629
 Qy 486 HHFNHVMILQSEGHNIFANLSKEYSDMLLKQSLATDLTLYFERRTEFFELVSKGE 545
 Db 630 HHLEFGTKLRDESLNIFQNLNRQHEHAHMDIAIATDLALYFKRTMFQKIVDQSK 689
 Qy 546 -----YDWN-----IKNRHDIERSMLTACDLGAVTKPWEISROVAELVTSERPEQDRE 595
 Db 690 TYESTQEWQYMMLEQTKKEIVMAMMTACDLSAITKPEWQSVKALLVAAEFWEQDGL 749
 Qy 596 RLEKLTPSAIFDRNRKDELPRLEWTDSTCMPLYQALVKNVYKLPKMLDSVATNRSK 655
 Db 750 RTVLQONPIMPMDRNKADLPKLVGFIDFVCTEYVYKEFSHFHEITPMLDGTNNRKEW 809
 Qy 656 -----EELHOKRELLASTASSSS 672
 Db 810 KALADEYAKMKALEEKKQQAQAASGN 840
 RESULT 8
 A47451
 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - dog
 C:Species: Canis lupus familiaris (dog)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
 C:Accession: A47451; S34290
 R:Suber, M.L.; Pittler, S.J.; Qin, N.; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 90, 3968-3972, 1993
 A:Title: Irish setter dogs affected with rod/cone dysplasia contain a nonsense mutation
 A:Reference number: A47451; MUID:93248211; PMID:8387203
 A:Accession: A47451
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-856 <SUB>
 A:Cross-references: GB:223014; NID:9312327
 A:Experimental source: Irish setter, retina
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:130782, NCBI:P130783)
 R:Clements, P.J.
 submitted to the EMBL Data Library, June 1993
 A:Reference number: S34290
 A:Accession: S34290
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-184, 'D', 186-856 <CLE>
 A:Cross-references: EMBL:223014; NID:9312327; PIDN:CA80557.1; PID:9312328
 C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
 C:Keywords: cGMP binding; phosphoric diester hydrolase
 F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <GNP>
 Query Match 29.2%; Score 1027; DB 1; Length 856;
 Best Local Similarity 34.3%; Pred. No. 8e-62;
 Matches 232; Conservative 124; Mismatches 243; Indels 78; Gaps 12;

Qy 46 LIQQTQTKRRFNDKIDKLTGYTKSLCMLPISRSGEILIGVAAQINKIPGAPFTEDD 105
 Db 148 MNVQDVTECHPFSFADELATGYETRNILATPIMNGK--EVAVIMALNKL--DGPCTFSD 205
 Qy 106 EKVQMQLPFCGIAISNAQLFAASRKEYSRALLVNVNDLFEQTDLEKIVKLIHRAQ 165
 Db 206 EDVFLKYLNFQTLNLKIYHLSYLHNCETRRGOVLLWSANKVFEELTDIERQHFKAFTVR 265
 Qy 166 TLLKRCRCSVLLLEDIESPVVKFTKSFEL-----MSPKCSADAENSF----- 207
 Db 266 AYLCNDRYSVGLD-----MTKEKEFFDVPVLMGEAQYSGPRTPDGRIVFYKVIDYI 320
 Qy 208 ---KESME--KSSYSD--WLINNSIAELVASTGLPNISDAYODPRFDAEADQI--SGPHI 259
 Db 321 LHGKEDIKVIKIPSPADHVALVSGLPYVAESGFCINIMNTAADENFTFEQGLDSDGWI 380
 Qy 260 RSVLCVPIWNSHQLIIGVAQVNLRLDGKPFDDADQRLFEAFVIFGGLGNNTIMYDQVKK 319
 Db 381 KNVLSMPTIVNKEEIVGVATFYNRKDGKPFDDQDEDEVUMESLTQFLGWSVLPNTDIDYRWNK 440
 Qy 320 SWAKOSVALDVLVSYHATCSKAEVDKFAA-----IPLVSELA 357
 Db 441 LENRKDTAQDMVLYHVRCDEIQILPTRELRKGPADCEDEELGILLKEVLPGSKFD 500
 Qy 358 IDDTDFDSDVDVAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNR 417
 Db 501 IYEFHFSDECTELEVKCGIQMYELGVKRFQIPQEVLVRFVLFPSKGYRRIYHNR 560
 Qy 418 HAFNVQMLFAMLTITAGFDQILTEVEILAVIVGCLDHRGTNNATQAKSGSLAQIY 477
 Db 561 HGFNVAQTMFTLLTGTGLKSYTDLQAFAMVYTAGLCHDIDHRTNNLYQMKSONPLAKLH 620
 Qy 478 GTSATLEHHHFNHVMILQSEGHNIFANLSKEYSDMLLKQSLATDLTLYFERRTEF 537
 Db 621 G--SSILERHLEFGKFLSSEETLNIYQNLNRQHEHVIHMDIAIATDLALYFKRTMF 679
 Qy 538 FELVSKGEYDWNINKNRD-----IFRSMIMTACDLGAVTKPWEISROVA 581
 Db 680 QKIVDES-----KNYEDRKSWEVLSLETTTRKEIVMAMMTACDLSAITKPEWQSKVA 733
 Qy 582 ELVTSERPEQDRELRKLTSPSAIFDRNRKDELPRLEWTDSTCMPLYQALVKNVYK 641
 Db 734 LLVAAEFWEQDGLERTVLDQOPIPMMDRNKAAELPKLVGFIDFVCTEYVYKEFSHFHEI 793
 Qy 642 KPMILDSVATNRSKWEEL 658
 Db 794 LPMEDRLQNNRKENKAL 810
 RESULT 9
 S06418
 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine
 N:Alternate names: cGMP phosphodiesterase alpha chain
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: S06418; S27007; S00161; A34611; S08516
 R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khrantsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.;
 T.M.; Bystrov, N.S.; Severtsova, I.V.; Lipkin, V.M.
 Dokl. Biochem. 296, 303-307, 1987
 A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the
 A:Reference number: S06418
 A:Accession: S06418
 A:Molecule type: mRNA
 A:Residues: 1-859 <OVI>
 A:Cross-references: EMBL:X12756; NID:9616; PIDN:CAA31243.1; PID:9617
 A:Accession: S27007
 A:Molecule type: protein
 A:Residues: 2-11; 22-27; 33-40; 95-98; 112-115; 180-193; 248-267; 275-282; 297-306; 312-330; 36
 645; 654-661; 663-667; 703-712; 734-736; 751-760; 766-771; 787-798; 811-819 <OVC>
 A:Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nau
 R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khrantsov, N.V.; Ishchenko, K.A.; Zagraniichny, V.E
 FEBS Lett. 223, 169-173, 1987
 A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the

A:Reference number: S00161; MUID:88030033; PMID:2822478

A:Accession: S00161

A:Molecule type: mRNA

A:Residues: 1-859 <OV2>

A:Cross-references: EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PID:g162828

A:Note: part of this sequence was confirmed by protein sequencing

A:Note: 381-Val was also found

R:Pittler, S.J.; Baehr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen,

Genomics 6, 272-283, 1990

A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi-

A:Reference number: A34611; MUID:90169986; PMID:2155175

A:Accession: A34611

A:Molecule type: mRNA

A:Residues: 1-193,'V',195-423,'T',425-674,'F',676-859 <PIT>

A:Cross-references: GB:M26043; NID:g162833; PIDN:AAA30443.1; PID:g162834

C:Comment: This protein is involved in the transduction and amplification of the visual

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide

C:Keywords: acetylated amino end; cGMP; heterotrimer; phosphoric diester hydrolase; retin-

F:2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <MA

F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental

Query Match 29.2%; Score 1026; DB 1; Length 859;

Best Local Similarity 32.6%; Pred. No. 9.4e-62;

Matches 225; Conservative 138; Mismatches 62; Indels 80; Gaps 12;

QY 54 KDRFENDEIDKLTGYKTSLLCMPIRSSDGEIIGVAQAINKIPECAPTEDEDEKVMOMYL 113

DB 158 EDEHCFDFVTLTEYQTKNILASPIMNGK-DVVAIMAVNKV-DGPHTEENDEELLKYL 215

QY 114 PCGTAISNAQLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKIMHRAQTLKLCRC 173

DB 216 NFNANLIMKVFHLSYLHNCETRRGQILLWSGKVFEEITDIERQFHKALYTVRAFLNCDRY 275

QY 174 SVLLLEDIESPVVKFTKSFEL-----MSPKCSADAENSF-----KESME 212

DB 276 SVGLLD-----MTKQKEFFDVPVLMGAPYPGRTPDGRIEINFKVIDILHGKEDIK 330

QY 213 ---KSSYSDWLNNISIAELVASTGLPVNISDAQDPREDAEADQI--SGFHRSVLCVPI 267

DB 331 VIPNPPDHVALVSLPTVYQAQGLICINIMNAPSEDFAFQKEPLDESQWIKNVLNPI 390

QY 268 WNSNHQIIGVAQVNLNLDGKPFDDADQRLFEAFVIFCGLGINTIMYDQVKHSAKQSV 327

DB 391 VNKKEEIVGVAIFYNRKDKGKPFDEMDETLMESLAQFLGWSVLNPDYELMKNLENRKDIF 450

QY 328 LDVLSYHATCSKAEDV-----KFKAAINPLVSELAIDDIHFD 365

DB 451 QDMVKYHKVCDNEEIQTILKTREYVYGKEPCEEEELAEILOGELPDADKYEINKFHFSD 510

QY 366 FSLVDAMITAAALRMFMELGMVQKFDIDYETLCRWLLTVRKNYRMVLYHNHRAFNVCOL 425

DB 511 LPLTELELVKGIQMYELKVVDFRHPHQEALVRFMYSLSKYRITVHNHGFNGVQT 570

QY 426 MFAMLTITAGFODILTEVEILAVIVCGCLCHDLDRGTNNNAFOAKSGSALQIYGTSATLEH 485

DB 571 MFSLVTVTKLRYFTDLEALAVMTAAAFCHDIDHRTNLYQMKSONPLAKLHG--SSILER 629

QY 486 HHENHAVMILQSEGNIFANLSKEYSDLMQLLQKSLATDLTYFFERTFEFFELVSKG- 544

DB 630 HHLFEGTKLLKDESUNFONLRHROHEAHIMMDIAIATDIALYCKRNTFKQIKVDQSK 689

QY 545 ----EYDWN-----IKNHRDIFRSMITACDLGAVTKPWEISROVAELVTSERFEQGDRE 595

DB 690 TYEQEOWTOYMLDQTRKEIVMAAMMTACDLSAITKPFWEVQSKVALLVAEFWEQGDLE 749

QY 596 RLEKLPTSAIFDRNRKDELPRLOLEWIDTSCMPLYQALVKVYKLPMLDSVATNRSKW 655

DB 750 RTVLQONPIMPDRNKADLPKLVGFDFVCTEYKEFSRFEHFEITPMLDGIITNRKEW 809

QY 656 -----EELHQKRLLASTSSSS 672

DB 810 KALADEYETKMKGLEEKQKQOAAANQAAAGS 840

RESULT 10

S30762

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000

C:Accession: S30762; S13031; S13121

R:Baehr, W.

submitted to the EMBL Data Library, June 1991

A:Reference number: S30762

A:Accession: S30762

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-856 <BAE>

A:Cross-references: EMBL:X60133; NID:g53595; PIDN:CAA42719.1; PID:g53596

R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.

FEBS Lett. 278, 107-114, 1991

A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase al

pha chain of the beta-subunit gene.

A:Reference number: S13030; MUID:91130581; PMID:1847109

A:Accession: S13031

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-559,'G',561-856 <BA2>

A:Cross-references: EMBL:X60133

R:Boxes, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.B.

Nature 347, 677-680, 1990

A:Title: Retinal degeneration in the rd mouse is caused by a defect in the beta subun

A:Reference number: S13121; MUID:91015387; PMID:1977087

A:Accession: S13121

A:Molecule type: mRNA

A:Residues: 1-2,'X',4,'G',6-18,'S',20-48,'DV',51-157,'T',159-175,'C',177-231,'R',233-

A:Cross-references: EMBL:X5968; NID:g53616; PIDN:CAA39439.1; PID:g53617

A:Note: the authors translated the codon AGA for residue 232 as Glu

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid

e; Keywords: cGMP binding; phosphoric diester hydrolase

F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 29.2%; Score 1025; DB 2; Length 856;

Best Local Similarity 34.1%; Pred. No. 1.le-61;

Matches 231; Conservative 121; Mismatches 247; Indels 78; Gaps 11;

QY 46 LIQRTKTKDRRDEIDKLTGYKTSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDD 105

DB 148 MINVDVAECCHFSFEADELTDYTKNLLSPIMNGK-DVVAVIMAVNKL-DGPCFTSED 205

QY 106 EKVQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKIMHRAQ 165

DB 206 EDVETKYNLNFATLNKTYHLSYLHNCETRRGQVLLWSANKVFEELTDIERQFHAKFYTVR 265

QY 166 TLLCERCSSVLLLEDIESPVVKFTKSFEL-----MSPKCSADAENSF----- 207

DB 266 AYLNCERYSGLLD-----MTKEKEFFDVPVLMGAEQAPYSGRTPDGRITVFYKVIDYI 320

QY 208 ---KESME---KSSYSDWLNNISIAELVASTGLPVNISDAQDPREDAEADQI--SGFHI 259

DB 321 LHGHEDIKVIPTPADHVALASGLPTVVAESGFTCNIMNASADEMFNFQEGPLDSDSGWVI 380

QY 260 RSVLCVPIMNSNHQIIGVAQVNLNLDGKPFDDADQRLFEAFVIFCGLGINTIMYDQVKK 319

DB 381 KNVLSMPTVNRKEEIVGVAIFYNRKDKGKPFDDQDEVLMESLTQFLGWSVLNPDYELMKNK 440

QY 320 SWAKQSVLDVLSYHATCSKAEDV-----KFKAAINPLVSELA 357

DB 441 LENRKKIAQDMVLYHVRCKDEIOEILPTRDLRGLKEPADCEDELGKILKEELPGTKFD 500

QY 358 IDDIHFDDESLDAMDALITAAALRMFMELGMVQKFDIDYETLCRWLLTVRKNYRMVLYHNHR 417

DB 501 IYEFHFDSECTELELVKCGIQMYELKVVDFRHPHQEALVRFMYSLSKYRITVHNHGFNGVQT 560

QY 418 HAFNVCOMLFAMLTITAGFODILTEVEILAVIVCGCLCHDLDRGTNNNAFOAKSGSALQIY 477


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Db 561 HGFNVAQWTFLLMTGKLSYYTDLEAFAMVTAGLCHDIDHRGTNNLYQMSQNPPLAKLH 620
Qy 478 GTSATLEHHHFNHNAVMIQSEGHNFANLSSKEYSDLMQLKQSLATLDTLYFFRRTEF 537
Db 621 G-SSILERHHLEFGKFLLAESLNIYQNLNRQHEHVHLMIDIAIATDLALYFKKRTMF 679
Qy 538 FELVSKGEYDNKIHNRD-----IFRSMLMTACDGLGAVTWPWEISROVA 581
Db 680 QKIVDES-----KNYEDKKSWVEYLSLETTKRKEIVMAMMTACDLSAITRPWEYSQKVA 733
Qy 582 ELVTSEFFEQDGRLEKLTPSAIFDRNRKDELPRLOLEWIDSTCMPLQALYKVNKL 641
Db 734 LLVAAREFWEQDLETVLDOQPIPMMDNRKAAELPKQVGFIDFVCTVYKFEFSRHEEI 793
Qy 642 KPMDSVATNRSKWBEEL 658
Db 794 LPMFDRLONNRKWKAL 810

RESULT 11
A42828
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A42828; S34590; S18715
R:Collins, C.; Hutchinson, G.; Kowbel, D.; Riess, O.; Weber, B.; Hayden, M.R.
Genomics 13, 698-704, 1992
A:Title: The human beta-subunit of rod photoreceptor cGMP phosphodiesterase: complete re
A:Reference number: A42828; UID:92347868; PMID:1322354
A:Accession: A42828
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-854 <CLR>
A:Cross-references: GB:S41458; NID:q252252; PIDN:AAB22690.1; PID:q252253
A>Note: sequence extracted from NCBI backbone (NCBIN:109783, NCBIIP:109784)
R:Khramtsov, N.V.; Feshchenko, E.A.; Suslova, V.A.; Shmukler, B.E.; Terpugov, B.E.; Raki
FEBS Lett. 327, 275-278, 1993
A:Title: The human rod photoreceptor cGMP phosphodiesterase beta-subunit. Structural stu
A:Reference number: S34590; UID:93351644; PMID:8394243
A:Accession: S34590
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-854 <KRR>
A:Cross-references: EMBL:X66142; NID:q396492; PIDN:CAA46932.1; PID:q396493
R:Weber, B.; Riess, O.; Hutchinson, G.; Collins, C.; Lin, B.; Kowbel, D.; Andrew, S.; S
Nucleic Acids Res. 19, 6263-6268, 1991
A:Title: Genomic organization and complete sequence of the human gene encoding the beta-
A:Reference number: S18715; UID:92066478; PMID:1720239
A:Accession: S18715
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314,'Q',316-319,'L',321-359,'R',361-697,'I',699-854 <WEB>
A:Cross-references: EMBL:X62694
C:Genetics:
A:Gene: GDB:PD56B; PDEB
A:Cross-references: GDB:125915; OMIM:180072
A:Map position: 4p16.3-4p16.3
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p
F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CMP>

Query Match 29.0%; Score 1020; DB 2; Length 854;
Best Local Similarity 34.4%; Pred. No. 2.4e-61;
Matches 229; Conservative 118; Mismatches 240; Indels 78; Gaps 11;

Qy 58 FNDEIDKLTGYKTSLLCMPRSSDGEILGVAQAINKIPEGAPFTEDEKVMQWMLPCG 117
Db 160 FSSFADELDTYKTNMLATPTMNGK-DYVAVIMAVNKL-NGFFFTSEDEDFVKYLNFEAT 217
Qy 118 IAINQAQLFAASRKEYSRALLEVVNDLFEOTDLEKIVKIMHRAOTLLKRCRCSVLL 177
Db 218 LYLKTIYHLSYHNCETRRGOVLLWSANKVFEELTDIERQFHAKFTYVRAYLNCERSYVGL 277
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Qy 178 LEDIESPVVKFTKSEFLMS-----PKCSADAENSF-----KESME---K 213
Db 278 LD-----MTKEKEFFDVMSLGMESQPSGPRTPDGRREIVFYKVIDYILHGREIKVIPT 332
Qy 214 SSSDWLNNLSIAELVASTGLPVNLSDAYQDPFRDAEADQI--SGFHRSILVCLVFNWSN 271
Db 333 PSADHWAASGLPSVAESGFGICNINNASADEMFKEQEGALDDSGWLKKNVLSMPTVKK 392
Qy 272 HQIIGVAQVNLRLDCKPFPDDADQRIFEAFVIFCGIGINNNTIMYDOVKKSWAKQSVALDVL 331
Db 393 BEIVGVATFYNRKDGKPFDEQDEVLMESITQFLGHVSVNTDITYDKMNKLENKDLAQDMV 452
Qy 332 SYHATCSKAEDVKFAANIPLVSELA-----IDDTHTDFDDESLD 369
Db 453 LYHVKCDRDEIQILPTRARLGKEPADCDEDELGEILKEELPGPTTFDIYEFHFSDELECT 512
Qy 370 VDMITAALRMPELMGMVKQPKIDYETLCRWLLTYRKKNYRMVLYHNHRIAFNVCOLMFAM 429
Db 513 ELDLVKCGIQMYEYELGVVKKFOIPQEVLVRFISKGYRRITYHNHRRHGFVNAQTMFTL 572
Qy 430 LTTAGFODILTVEVILAVIVGCLCHDLHRGTNNAFOAKSGSALAOQLYCTSATLEHHFN 489
Db 573 LMTGKLSYYTDLFAFAMVTAGLCHDIDHRGTNNLYQMSQNPPLAKLHG-SSILERHLE 631
Qy 490 HAVMILOSEGHNFANLSSKEYSDLMQLKQSLATLDTLYFFRRTEFFELYSKGEYDWN 549
Db 632 FGKFLSEETLNIYQNLNRQHEHVHLMIDIAIATDLALYFKKRAMFOKIVDES----- 686
Qy 550 IKNHRD-----IFRSMLMTACDGLGAVTWPWEISROVAELVTSSEFFEQGD 593
Db 687 -KNYQDKKSWVEYLSLETTKRKEIVMAMMTACDLSAITKPWEVQSKVALLVAAEFWEQGD 745
Qy 594 RERLELKUTPSAIFDRNRKDELPRLOLEWIDSTCMPLQALYKVNKLKPMDSVATNRS 653
Db 746 LERTVLDQOPIPMMDNRKAAELPKQVGFIDFVCTVYKFEFSRHEEILPMPDRLONNRK 805
Qy 654 KWEEL 658
Db 806 EWKAL 810

RESULT 12
A36617
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - bovine
N:Alternate names: cGMP phosphodiesterase beta chain
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 21-Jan-2000
C:Accession: A36617; S19145; S14011; S00251
R:Lipkin, V.M.; Khramtsov, N.V.; Vasilevskaya, I.A.; Atabekova, N.V.; Muradov, K.G.;
J. Biol. Chem. 265, 12955-12959, 1990
A:Title: Beta-subunit of bovine rod photoreceptor cGMP phosphodiesterase. Comparison
A:Reference number: A36617; UID:90330632; PMID:2165490
A:Accession: A36617
A:Molecule type: mRNA
A:Residues: 1-853 <LIP>
A:Cross-references: GB:J05553; NID:g162824; PIDN:AAA30440.1; PID:g162825
A:Experimental source: retina
A>Note: 40-Arg was also found
R:Lipkin, V.
submitted to the EMBL Data Library, December 1990
A:Reference number: S19145
A:Accession: S19145
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-853 <LIP>
A:Cross-references: EMBL:X57146; NID:g209; PIDN:CAA40436.1; PID:g210
R:Lipkin, V.M.; Gubanov, V.V.; Khramtsov, N.V.; Vasilevskaya, I.A.; Atabekova, N.V.;
Blaug, Khim. 16, 118-120, 1990
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the
A:Reference number: S14011; UID:90267525; PMID:2161230
A:Accession: S14011
A>Status: preliminary
A:Molecule type: mRNA
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3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta' chain - mouse
C:Species: Mus musculus (house mouse)

C>Date: 26-Aug-1999 #sequence-revision 26-Aug-1999 #text_change 05-Nov-1999
C/Accession: A40981; B36112; A36112; B26650; A60179; C26650
R/Sonnenburg, W.K.; Mullaney, P.J.; Beavo, J.A.
J. Biol. Chem. 266, 17655-17661, 1991
A>Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiesterase
A/Reference number: A40981; MUID:91373395; PMID:1654333
A/Accession: A40981
A/Molecule type: mRNA
A/Residues: 1-921 <SON>
A/Cross-references: GB:M73512; NID:g162829; PIDN:AAA74559,1; PID:g162830
R/Le Trong, H.; Beier, N.; Sonnenburg, W.K.; Stroop, S.D.; Walsh, K.A.; Beavo, J.A.;
Biochemistry 29, 10280-10288, 1990
A/Title: Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodiesterase
A/Reference number: A36112; MUID:91104948; PMID:2176866
A/Accession: B36112
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 592-921 <LET>
A/Accession: A36112
A/Molecule type: protein
A/Residues: 1-203, 'D', '205-477', 'Q', '479-921 <LET>
R/Charbonneau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9308-9312, 1986
A/Title: Identification of a conserved domain among cyclic nucleotide phosphodiesterases
A/Reference number: A26650; MUID:87092242; PMID:3025833
A/Accession: B26650
A/Molecule type: protein
A/Residues: 613-632, 'L', '634-794; 808-868 <CHA>
A/Experimental source: heart
R/Tanaka, T.; Hockman, S.; Moos Jr., M.; Taira, M.; Meaccl, E.; Murashima, S.; Mangan
Second Messengers Phosphoproteins 13, 87-98, 1991
A/Title: Comparison of putative cGMP-binding regions in bovine brain and cardiac cGMP
A/Reference number: A60179; MUID:92065414; PMID:1659635
A/Accession: A60179
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 311-803, 'DV', '806-921 <TAN>
A/Note: part of this sequence was confirmed by protein sequencing
C/Comment: This protein is not glycosylated.
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-
C/Keywords: acetylated amino end; alternative splicing; cAMP binding; cGMP binding; cGMP
F/635-857/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F/1/Modified site: acetylated amino end (Met) #status experimental

Query Match	26.2%	Score	920.5	DB	1	Length	921;		
Best Local Similarity	32.8%	Pred.No.	1	6e-54;					
Matches	210;	Conservative	130;	Mismatches	254;	Indels	47;	Gaps	12;

Qy	48	QROTKTKDRFND--ETDKLTGYTKSLLCMPI--RSSDGEIIGVAQAINKIPEGAPFTE	103
Db	283	KKSILQLDLTSDMQLOSLMLGCEVQAMLCVPVISRATD-QVVVALACAFNKL-GGDLFTD	340
Qy	104	DDEKVWMYLPFGCIAISNAQLFAASRKYERSRALLVVDNLFPEQTDLEKIVKIMHR	163
Db	341	QDEHVIOHCFFHYTSTVLTTSLAFQKCEQALLQVAKNLFTHLDDVSVLLQEIITE	400
Qy	164	AQTLKCCERCSVLLEDDIESPVVKF-----TKSFFELMSPKCSADAENSEKSEKSSYS	217
Db	401	ARNLSNAETCSVFLLDQNELVAKVFGGVVEDESYEIRP-----	440
Qy	218	DWLINNSIAELVASTGLPVNISDAYQDPRFDAADQISGFHRSVLCVPINSHQILGV	277
Db	441	--ADQIAGHVATTGQILNIPDAYAHLPLYRGVDDSTGFRTRNILCFPIKNENQEVIGV	497
Qy	278	AQVNLRLDGKPFDDAQRLEPEAFVIFGGLGINNTIMYDQVKKSNAKOSVALDVLVSYHATC	337
Db	498	AELVNKINGPWFSEKFDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYIMKV	557
Qy	338	SKAEVDKFAANIPLVSELAIDDIHEDDF-----SLDVDAMITTAALRMFMELGNVOKFKI	392
Db	558	SDEYTKLLHDGTOPAAI---DSNFASFYTPRSLPEDDTSMAILSMLQDMFNINNYKI	614
Qy	393	DYETLCRWLTLTRKNYRMVLIHNHRAFNVCOLMEAMFLTATAGFODILTEVEILAVIVGCL	452

3', 5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine
 N:Alternate names: cGMP-dependent phosphodiesterase
 C:Species: Bos primigenius taurus (cattle)

Db 615 DCPTLARECLVYKGYRDPYPYHNWMAFVSFHCYLLYKNLELTNYLEDMEIFALFISCM 674
QY 453 CHDLDRGTNNAFAQKSGSALAQLYGT-SATLEHHHHNHNHAYMILOSEGHNIFANLSKEY 511
Db 675 CHDLDRGTNNSFQVASKSVLAALYSSEGSVNERHHFAOIAILNTHGNCNIFDHFSCRKY 734
QY 512 SDLMOLLKQSIIATDLYFERRTEFFELVSKGEYDWNINKNHRDIFRSMLMTACDLGAVT 571
Db 735 QRMULDLMRDIIILATDLAHLRIFRDLOKMAEVG-YDRTNKQHHSLLLCLLMTSCDLSQDT 793
QY 572 KPWEISROVAELVTSEFPEQGDRELEKLTPSAIFDRNRKDELPRLOLEWIDSTCMPLY 631
Db 794 KGWKTTRKIAELLYKEFFSQGDLEK-AMGNRPMMMDR-EKAYIPELOISEMEHIAMPIY 851
QY 632 QALVKVNVKLPMLDSVATNRSKWEELHOKRLLASTASSSS 672
Db 852 KLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNS 892

Search completed: June 13, 2003, 15:49:42
Job time : 44.4875 secs

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:38:49 ; Search time 14.0228 seconds
(without alignments)
2023.123 Million cell updates/sec

Title: US-09-663-542-1

Perfect score: 3516

Sequence: 1 MLKQARPLFRNLSATQWK.....ASTASSSPASVMVAKEDRN 684

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1366.5	38.9	875	1 CNSA_HUMAN	076074 homo sapien
2	1357.5	38.6	865	1 CNSA_CANFA	077746 canis famil
3	1355.5	38.6	865	1 CNSA_BOVIN	Q28156 bos taurus
4	1352	38.5	833	1 CNSA_RAT	054735 rattus norv
5	1060	30.1	862	1 CNRC_CHICK	P52731 gallus gall
6	1047.5	29.8	859	1 CNSA_HUMAN	P16499 homo sapien
7	1039.5	29.6	855	1 CNRC_BOVIN	P16586 bos taurus
8	1030	29.3	858	1 CNRA_BOVIN	P11541 bos taurus
9	1030	29.3	858	1 CNRA_MOUSE	P27664 mus musculu
10	1029.5	29.3	858	1 CNRC_HUMAN	P51160 homo sapien
11	1024	29.1	856	1 CNRB_CANFA	P33726 canis famil
12	1020	29.0	854	1 CNRB_HUMAN	P35913 homo sapien
13	1020	29.0	856	1 CNRB_MOUSE	P23440 mus musculu
14	1019	29.0	860	1 CNRA_CANFA	Q28263 canis famil
15	1009	28.7	853	1 CNRB_BOVIN	P23439 bos taurus
16	950	27.0	779	1 CN10_HUMAN	Q9Y233 homo sapien
17	934.5	26.6	941	1 CN2A_HUMAN	Q00408 homo sapien
18	933.5	26.6	928	1 CN2A_RAT	Q01062 rattus norv
19	920.5	26.2	921	1 CN2A_BOVIN	P14099 bos taurus
20	790	22.5	933	1 YBZJ_CAEEL	P91119 caenorhabdi
21	573.5	16.3	365	1 CNSA_MOUSE	Q92284 mus musculu
22	535.5	15.2	918	1 YNF6_CAEEL	P30645 caenorhabdi
23	451.5	12.8	793	1 REGA_DICDI	Q23917 dictyosteli
24	443.5	12.6	534	1 CNSA_MOUSE	Q70628 mus musculu
25	421	12.0	593	1 CNSA_HUMAN	Q76083 homo sapien
26	381	10.8	536	1 CN4C_RAT	P14644 rattus norv
27	369	10.5	712	1 CN4C_HUMAN	Q08493 homo sapien
28	364	10.4	809	1 CN4D_HUMAN	Q08499 homo sapien
29	362.5	10.3	844	1 CN4A_RAT	P54748 rattus norv
30	362.5	10.3	886	1 CN4A_HUMAN	P27815 homo sapien
31	362	10.3	672	1 CN4D_RAT	P14270 rattus norv
32	331	10.0	446	1 CN7B_MOUSE	Q9QXQ1 mus musculu
33	350	10.0	535	1 CN1B_MOUSE	Q01065 mus musculu

ALIGNMENTS

RESULT 1

ID	CNSA_HUMAN	STANDARD;	PRT;	875 AA.
AC	076074; 075887; 075026; Q9Y626;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)			
DE	(CGMP-binding CGMP-specific phosphodiesterase).			
GN	PDE5A OR PDE5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM PDE5A1 AND PDE5A2).			
RX	MEDLINE=98382582; PubMed=9714779;			
RA	Loughney K., Hill T.R., Florio V.A., Uher L., Rosman G.J., Wolda S.L.,			
RA	Jones B.A., Howard M.L., McAllister-Lucas L.M., Sonnenburg W.K.,			
RA	Francis S.H., Corbin J.D., Beavo J.A., Ferguson K.;			
RT	"Isolation and characterization of cDNAs encoding PDE5A, a human CGMP-			
RT	binding, CGMP-specific 3',5'-cyclic nucleotide phosphodiesterase.";			
RL	Gene 216:139-147(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM PDE5A1).			
RX	TISSUE=Placenta, and Lung;			
RX	MEDLINE=98380237; PubMed=9716380;			
RA	Yanaka N., Kotera J., Ohtsuka A., Akatsuka H., Imai Y., Michibata H.,			
RA	Fujishige K., Kawai E., Takebayashi S.-I., Okumura K., Omori K.;			
RT	"Expression, structure and chromosomal localization of the human			
RT	CGMP-binding CGMP-specific phosphodiesterase PDE5A gene.";			
RL	Eur. J. Biochem. 255:391-399(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM PDE5A1).			
RP	TISSUE=Prostate, and Skeletal muscle;			
RX	MEDLINE=98308101; PubMed=9642111;			
RA	Stacey P., Ruten S., Dapling A., Phillips S.C.;			
RT	"Molecular cloning and expression of human CGMP-binding CGMP-specific			
RT	phosphodiesterase.";			
RL	Biochem. Biophys. Res. Commun. 247:249-254(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM PDE5A2).			
RC	TISSUE=Lung;			
RA	Kotera J., Imai Y., Omori K.;			
RT	"Molecular cloning and characterization of human CGMP-specific			
RT	phosphodiesterase 5A2 cDNA.";			
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE			
CC	INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS			
CC	PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-			
CC	GMP.			
CC	-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =			
CC	guanosine 5'-phosphate.			
CC	-!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR			
CC	MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT			
CC	CATALYSTS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).			

34	350	10.0	535	1 CN1B_RAT	Q01066 rattus norv
35	349	9.9	456	1 CN7A_MOUSE	P70453 mus musculu
36	349	9.9	721	1 CN4B_RAT	P14646 rattus norv
37	347	9.9	482	1 CN7A_HUMAN	Q13946 homo sapien
38	346	9.8	426	1 CN7A_RAT	Q08593 rattus norv
39	346	9.8	450	1 CN7B_HUMAN	Q9np56 homo sapien
40	345	9.8	736	1 CN4B_HUMAN	Q07343 homo sapien
41	342.5	9.7	534	1 CN1B_BOVIN	Q01061 bos taurus
42	340	9.7	709	1 CN1C_HUMAN	Q14123 homo sapien
43	338.5	9.6	549	1 YST1_CAEEL	Q22000 caenorhabdi
44	338	9.6	536	1 CN1B_HUMAN	Q01064 homo sapien
45	337.5	9.6	654	1 CN1C_MOUSE	Q64338 mus musculu

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
CC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS PDE5A1 AND PDE5A2).
RC TISSUE=Lung;
RA MEDLINE=98434620; PubMed=9756948;
RX Katsura J., Fujishige K., Akatsuka H., Imai Y., Yanaka N., Omori K.;
RT "Novel alternative splice variants of cGMP-binding cGMP-specific
phosphodiesterase.";
RL J. Biol. Chem. 273:26982-26990(1998).
CC -!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
CC INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
CC PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-
CC GMP.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
CC MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT
CC CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).
CC -!- ENZYME REGULATION: INHIBITED BY ZAPRINAST.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- SUBCELLULAR LOCATION: PDE5A1 AND PDE5A2 ARE LOCATED MOSTLY TO
CC SOLUBLE CELLULAR FRACTIONS AND SOME TO PARTICULATE CELLULAR
CC FRACTIONS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PDE5A1 (SHOWN HERE) AND PDE5A2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: BOTH ISOFORMS EXPRESSED ABUNDANTLY IN THE
CC CEREBELLUM, HIPPOCAMPUS, RETINA, LUNG, HEART, SPLEEN, AND THORACIC
CC ARTERY. PDE5A1, BUT NOT PDE5A2, IS ALSO ABUNDANTLY EXPRESSED IN
CC THE PYLORUS.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
CC WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
CC AND B.
CC -!- PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
CC ALLOSTERIC SITES (BY SIMILARITY).
CC -!- MISCELLANEOUS: CGMP-BINDING TO THE ALLOSTERIC SITES IS STIMULATED
CC BY 3-ISOBUTYL-1-METHYLXANTHINE (IBMX).
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB008467; BAA33503.1; -
DR EMBL; AB008468; BAA33504.1; -
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolyase; cGMP; cGMP-binding; Phosphorylation; Alternative splicing;
Zinc; Repeat.
FT NP_BIND 228 311 CGMP (BY SIMILARITY).
FT NP_BIND 410 500 CGMP (BY SIMILARITY).
FT BINDING 276 276 CGMP (BY SIMILARITY).
FT BINDING 277 277 CGMP (BY SIMILARITY).
FT BINDING 289 289 CGMP (BY SIMILARITY).
FT BINDING 478 478 CGMP (BY SIMILARITY).
FT DOMAIN 578 843 CATALYTIC (BY SIMILARITY).
FT MOD_RES 92 92 PHOSPHORYLATION (POTENTIAL).
FT METAL 603 603 ZINC 1 (POTENTIAL).
FT METAL 607 607 ZINC 1 (POTENTIAL).

FT	METAL	632	632	ZINC 1 (POTENTIAL).
FT	METAL	643	643	ZINC 2 (POTENTIAL).
FT	METAL	647	647	ZINC 2 (POTENTIAL).
FT	METAL	672	672	ZINC 2 (POTENTIAL).
FT	VARSPPLIC	1	40	MERGSFGAARLPRDQDSVEAWLDDHRRDTFTSFYVKKAT -> MLPFGHQR (IN ISOFORM PDE5A2).
SO	SEQUENCE	865 AA;	98293 MW;	F20BB37B71E93BB6 CRC64;
	Query Match	38.6%;	Score 1357.5;	DB 1; Length 865;
	Best Local Similarity	42.9%;	Pred. No. 5.3e-83;	
	Matches	278;	Conservative 129;	Mismatches 190; Indels 51; Gaps 11;
Oy	54	KDRFNEIDKLGYKTKSLICMPIRSDGIIIGVAQAIN-KIEGAPPTDEDDKVMQMY	112	
Db	237	EDPRFAEVDQITGYKTSILCMPIKNHRREVGVQAQIKSGNGGTFTKDEKFAAY	296	
Oy	113	LPFGGIAISNOLFAASRKEVERSRALLEVVNDLFEQTDLEKIVKTMHRAQTLKKER	172	
Db	297	LAFGCVLHNALQYETSLLENKRNQVLDLASLIFEQOQSLEVLKKAATIIISFMQVOK	356	
Oy	173	CSVLLEIDIESPVVVKFTKSPKSGSADAENSFK-----ESMEKSSYSQWL-----	220	
Db	357	CTIIVDE-----DCSDSFSSVFHMECELEKLPDLTLRERDAN	395	
Oy	221	-INNSIAELVASTGIPVNSIDAYQDPRF---DADAQISGPHIRSVLCVPIWN-SNHQII	275	
Db	396	RINTMYAQYKNTMEPLNIPDVSXDKRPPMTNNTGNVQOCIRSLCTPIKNGKKNKI	455	
Oy	276	GVAQVLRNLDG-----KPFDDADQRLFEAFVIFCGLGINTIMYDQVKKWAKOSVALDV	330	
Db	456	GVCOLVKNMEENTGKVPFNRENDEQFLFAFVIFCGLGIONTQMYEAVERAWAKOMVTLEV	515	
Oy	331	LSYHATCSKABVDKFK---AANIPLVSELAIDDDTHFDDFSLDQVDMITAALRMFMELGMV	387	
Db	516	LSYHASAAEETKELQSLAAAVPSAQTLLKTDTSFSDLSLETALCTIRMTDLNV	575	
Oy	388	QKFIDYETLCRWLLTVRKNYRM-VLYHNWRHAFNVCOLMFAMITTAGFDILTEVEILA	446	
Db	576	QNFQMKHEVLCRWILSVKKNYKKNVAVYHNWRHAFNVCOLMFAMITTAGFDILTEVEILA	635	
Oy	447	VIVGCLCHLDHRTNNAFOAKSGSALAQLYGTSTATLEHHHFNHVMITLOSEGHNFANL	506	
Db	636	LLIAALSHDLDRGVNNSYIQRSEHPLAQLY-CHSIMEHHHFDQCLMILNPGNOILSGL	694	
Oy	507	SSKEYSDLMQLLKOSILATDLTLFPERTEFFELVSKGEYDWNINKNHRDIFRSMILMTACD	566	
Db	695	SIEEYKTLKIIKQAILATDLALYIKRGEFFELIRKNQFNLEDPHQKELFLAMLMTACD	754	
Oy	567	LGAVTKPWEISQVAELVTSFEFGDRERLEKLTPSAIFDRNRKDELPRQLQEWIDSI	626	
Db	755	LSAITKPWPIQORIAELVATEFFQDGRERKELNTEPADLNRKKNKIPSMQVGFDAI	814	
Oy	627	CMPLYQALVKVNVKLKPMLDVATNRSKWEEL--HOKRELLASTASSSS	672	
Db	815	CLQYEAHTVSEDCFPULDGCRNRKQKWAQAEQOEKTLINGESSQA	862	

RESULT 3
CN5A_BOVIN
ID CN5A_BOVIN STANDARD; PRT; 865 AA.
AC Q28156;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
DE (cGMP-binding cGMP-specific phosphodiesterase).
GN PDE5A OR PDE5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=94043054; PubMed=8226796;
RA McAllister-Lucas L.M., Sonnenburg W.K., Kadlecck A., Seger D.,
RA Trong H.L., Colbran J.L., Thomas M.K., Walsh K.A., Francis S.H.,
RA Corbin J.D., Beavo J.A.;
RT "The structure of a bovine lung cGMP-binding, cGMP-specific
RT phosphodiesterase deduced from a cDNA clone.";
RL J. Biol. Chem. 268:22863-22873(1993).
RN [2]
RN METAL-BINDING.
RP MEDLINE=94357882; PubMed=8077192;
RX Francis S.H., Colbran J.L., McAllister-Lucas L.M., Corbin J.D.;
RA "Zinc interactions and conserved motifs of the cGMP-binding cGMP-
RT specific phosphodiesterase suggest that it is a zinc hydrolase.";
RL J. Biol. Chem. 269:22477-22480(1994).
RN [3]
RN MUTAGENESIS.
RP MEDLINE=96107229; PubMed=8530505;
RX McAllister-Lucas L.M., Haik T.L., Colbran J.L., Sonnenburg W.K.,
RA Seger D., Turko I.V., Beavo J.A., Francis S.H., Corbin J.D.;
RT "An essential aspartic acid at each of two allosteric cGMP-binding
RT sites of a cGMP-specific phosphodiesterase.";
RL J. Biol. Chem. 270:30671-30679(1995).
RN [4]
RN MUTAGENESIS.
RP MEDLINE=96355629; PubMed=8703039;
RX Turko I.V., Haik T.L., McAllister-Lucas L.M., Burns F., Francis S.H.,
RA Francis S.H., Corbin J.D.;
RT "Identification of key amino acids in a conserved cGMP-binding site of
RT cGMP-binding phosphodiesterases. A putative NRXnd motif for cGMP
RT binding.";
RL J. Biol. Chem. 271:22240-22244(1996).
RN [5]
RN PHOSPHORYLATION, AND MUTAGENESIS.
RX MEDLINE=98109724; PubMed=9445376;
RA Turko I.V., Francis S.H., Corbin J.D.;
RT "Binding of cGMP to both allosteric sites of cGMP-binding cGMP-
RT specific phosphodiesterase (PDE5) is required for its
RT phosphorylation.";
RL Biochem. J. 329:505-510(1998).
CC -!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
CC INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
CC PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-
CC GMP.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
CC MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT
CC CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS.
CC -!- ENZYME REGULATION: MOST POTENTLY INHIBITED BY ZAPRINAST AND
CC DIPYRIDAMOLE.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
CC WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
CC AND B.
CC -!- PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
CC ALLOSTERIC SITES.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
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CC -----
CC EMBL: L16545; AB00990.1;
CC InterPro: IPR003018; GAF:
CC InterPro: IPR003607; ME_Pplase_Hdc.

DR InterPro: IPR002073; PDEase.
DR Pfam: PF002233; PDEase; 1.
DR Pfam: PF01590; GAF; 2.
DR PRINTS: PRO0387; PD1ESTERASE1.
DR SMART: SM00065; GAF; 2.
DR SMART: SM00471; Hdc; 1.
DR PROSITE: PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; cGMP-binding; Phosphorylation; zinc; Repeat.
FT MOD_RES 92 92
FT METAL 603 603
FT METAL 607 607
FT METAL 632 632
FT METAL 643 643
FT METAL 647 647
FT METAL 672 672
FT NP_BIND 228 311
FT NP_BIND 410 500
FT BINDING 276 276
FT BINDING 277 277
FT BINDING 289 289
FT BINDING 478 478
FT DOMAIN 578 843
FT MUTAGEN 276 276
FT MUTAGEN 277 277
FT MUTAGEN 277 277
FT MUTAGEN 277 277
FT MUTAGEN 289 289
FT MUTAGEN 289 289
FT MUTAGEN 290 290
FT MUTAGEN 478 478
FT MUTAGEN 478 478
SQ SEQUENCE 865 AA; 98626 MW; 2FF7144B2990B4F7 CRC64;
Query Match 38.6%; Score 1355.5; DB 1; Length 865;
Best Local Similarity 42.9%; Pred. No. 7.2e-83;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;
QY 54 KDRFNDEIDKLTGYTKSLCMLPIRSDEGIIIGVAQAQIN-KIPEGAPFTEDDEKVMQMY 112
DB 237 EDPRFNAEVQJITGYKTOSTLCMPKKNHREVGVAQAINKSGNGTFTTEKDEKFAAY 296
QY 113 LPFCGIAISNAOLFASRKEYERSRALLEVVNDLFEEOTDLEKIVKIMHRAQTLLKCE 172
DB 297 LAFCGIVLHNAQLYETSLLENKRNQVLLDLASLIFEQQQSLEVLKKAATIIISFMQVOK 356
QY 173 CSVLLLEDIESPVVKFTKSPKSPKSAENSFK-----ESMEKSSYSDWL----- 220
DB 357 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTRERD 393
QY 221 ---INNSIAELVSTGLPVNISDAYODPRDAEADQISGFH---IRSVLCVPIWN-SNHQ 273
DB 394 ANRINYAQVVKNTMEPLNIPDVSKDKRPWTNENMGNIQQCIRSLCTPIKNGKKNK 453
QY 274 IIGVAQVNLRLDG-----KPFDDADQRLPFAVIFCGIGLGINNTIMYDQVKSWAKQSVAL 328
DB 454 VIGVCQLVNKMEETTKGVKAFNRNDEQFLFAVIFCGIGLQNTQMYEAVERAMAKQMTL 513
QY 329 DVLSYHATCSK---AEVDKFKAAIPLVSELAITDIDHDFDVLSDVDAMITAAALRMFMELG 385
DB 514 EVLSYHAAEEETRELQSLAAAVPSAQTLLKIDTDFSEFSELSDELTAICTIRMTDLN 573
QY 386 MVQKFKIDYETLCRWLLTIVRKNYRM-VLYHNHRHAFNVQCLMFAMLTAGQDILTVEVI 444
DB 574 LVQNFQMKHEVLCKWILSVKKNYKNAVYHNRHAFNTAQCMFAALKAGKIKQKRLTDEI 633
QY 445 LAVIVGCLCHDLDRGTNNNAFOAKSGSALAQYCTSATLEHHHFNHNAVMILOSSEHNIFA 504
DB 634 LALLIAALSHDLDRGVNNSYIQRSEHPALQY-CHSIMEHHHFDQCLMILNSPGNQTL 692


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Qy 505 NLSKEYSDMLKQSLATDLTYFERRTEFFELVSKGYDWNKNIHRDIFRMLMTA 564
Db 693 GLSTEYKTLIIKQAILDALYIKRRGEFFELIMKNQFNEDPHOKELFLAMLMTA 752
Qy 565 CDLGAVKPKWEISRQVAELVTSSEFFEQDRELERLEKLTPTSAIFDRNRKDELPRQLQEWID 624
Db 753 CDLSAITKWPQIQRIAEIVATEFFQDGRKERKELNIEPADLMNREKKNKIPSNQVGFID 812
Qy 625 SICPLQALYKVNKVLKPLMDLSVATNRKWEEL--HOKRLLASTASSSS 672
Db 813 AICLQYEAETHVSDCEPFLDGCGRKNQKQWALAEQOEKTLINGESSQT 862

RESULT 4
CNSA_RAT STANDARD; PRT; 833 AA.
AC 054735;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
DE (CGMP-binding CGMP-specific phosphodiesterase).
GN PDE5A OR PDE5
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lung;
RX MEDLINE=98036118; PubMed=9370351;
RA Kotera J., Yanaka N., Fujishige K., Imai Y., Akatsuka H., Ishizuka T.,
RA Kawashima K., Omori K.;
RT "Expression of rat CGMP-binding CGMP-specific phosphodiesterase mRNA
RT in Purkinje cell layers during postnatal neuronal development.";
RL Eur. J. Biochem. 249:434-442(1997).
CC -! FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
CC INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
CC PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-
CC GMP.
CC -! CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate
CC -! COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
CC MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT
CC CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).
CC -! PATHWAY: Cyclic nucleotide metabolism.
CC -! ALTERNATIVE PRODUCTS: 2 ISOFORMS: PDE5A1 AND PDE5A2 (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -! DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
CC WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
CC AND B.
CC -! PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
CC ALLOSTERIC SITES (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D89093; BAA23672.1; .
CC InterPro: IPR003018; GAF.
CC InterPro: IPR003607; ME_Plpase_Hdc.
CC InterPro: IPR002073; PDEase.
CC Pfam: PF00233; PDEase; 1.
CC Pfam: PF01590; GAF; 2.
CC PRINTS: PR00387; PDIESTERASE1.
CC SMART; SM00065; GAF; 2.
```

```
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolyase; CGMP; CGMP-binding; Phosphorylation; Alternative splicing;
FT Zinc; Repeat
FT NP_BIND 196 279 CGMP (BY SIMILARITY).
FT NP_BIND 378 468 CGMP (BY SIMILARITY).
FT BINDING 244 244 CGMP (BY SIMILARITY).
FT BINDING 245 245 CGMP (BY SIMILARITY).
FT BINDING 257 257 CGMP (BY SIMILARITY).
FT BINDING 446 446 CGMP (BY SIMILARITY).
FT DOMAIN 546 811 CATALYTIC (BY SIMILARITY).
FT MOD_RES 60 60 PHOSPHORYLATION (POTENTIAL).
FT METAL 571 571 ZINC 1 (POTENTIAL).
FT METAL 575 575 ZINC 1 (POTENTIAL).
FT METAL 600 600 ZINC 1 (POTENTIAL).
FT METAL 611 611 ZINC 2 (POTENTIAL).
FT METAL 615 615 ZINC 2 (POTENTIAL).
FT METAL 640 640 ZINC 2 (POTENTIAL).
SQ SEQUENCE 833 AA; 94556 MW; 712DC159C80CB09D CRC64;

Query Match 38.5%; Score 1352; DB 1; Length 833;
Best Local Similarity 43.8%; Pred. No. 1.2e-82;
Matches 275; Conservative 129; Mismatches 198; Indels 26; Gaps 10;

Qy 54 KDRFNDEIDKLTGYTKSLCLMPISRSDDGRIIGVQAQIN-KIPEGAPFTEDEKVMQMY 112
Db 205 EDPREAEVDQITGYKTQSILCMPIKNHREEVGVQAQINKKSGNGGTFTEKDEKDFAA 264
Qy 113 LPFCGIAISNAQLFAASRKEYERSPALLEVNDLFEEOQTDLEKIVKIMHRAOTLLKCE 172
Db 265 LAFCGIVLHNAQLYETSLLENKRNQVLDLASFEEQSQSLEVLKKTAAATISPMQVOK 324
Qy 173 CSVLLEIDIESPVVVKTKSFELMSPKCSADASEFKESMEKSSYSDWLNNISIAELVAST 232
Db 325 CTIIVD--EDCPDSFSRVFQMEWEVCKSEPLTREHANK-----INTVAYQVYKNT 376
Qy 233 GLPNVISDAYODPRP---DAEADQISGPHIRSVLCVPIWN-SNHOIGVAVQLNRLDG-- 286
Db 377 MEPLNIPDVTNDRFPWTNNENGHINTHCIRSLCTPIKNGKKNKVGVCQLVKNMKEKT 436
Qy 287 ---RPFDADQORLEAFVIFCGLGGINNTIMDOYKKSNKAKOSVALDVLVSIATCSAEVD 343
Db 437 GKIRAFNQNDEQFLAEAFVIFCGLGIGNTQMYEAVERAMAKOMVTLEVISYHASAAEBET 496
Qy 344 KFK---AANIPLVSELAIDDDHFDQSLDVDAITAAALRMFMELGMVQKFKIDYETLCRW 400
Db 497 ELQALAAAVVESAQTLKITDFSFDFSLDLETALCTIRMTDLNLVQNFQMKHEVLCRW 556
Qy 401 LLTVRKNTVM-VLYHNWRHAFNVQOLMFAMLTTAGFDILTEVEILAVIVGCLCHDLDR 459
Db 557 ILSVKKNYKKNVAVHNWRHAENTACQMPAALKAGKIQNKLTDLDTLALLIALSHDLDR 616
Qy 460 GTNNAFOAKSALAAQLYGTSTATLEHHHFNHNAVILQSEGHNIFANLSKSEYSDLMQLLK 519
Db 617 GVNNSYQORSEHPLAQLY-CHSTMHHHFDQCLVMVNLSPGNQILSGLSIEEYKTKTLTK 675
Qy 520 QSILATDLTYFERTEFFELVSKGYDWNKNIHRDIFRMLMTACDLGAVTKPWEISRO 579
Db 676 QAILATDLALYIKRRGEFFELIRKNEFSFEDPQLOKELFLAMLMTACDLGAVTKPPIOR 735
Qy 580 VAEIVTSFEFFQDGRERLEKLTPTSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALYKVN 639
Db 736 IAEIVAAEFFQDGRERKELNIEPADLMNREKKNKIPSNQVGFIDICLQYEAETHVSE 795
Qy 640 KLKPLMDLSVATNRKWEEL---HOKRLL 664
Db 796 DCLPLDGCGRKNQKQWALAEQOEKTL 823

RESULT 5
CNSC_CHKCK
ID CNSC_CHKCK
AC P52731;
PRT; 862 AA.
```



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DR Pfam: PF00233; PDEase; 1.
DR Pfam: PF01590; GAF; 2.
DR PRINTS: PR00387; PDIESTERASE1.
DR SMART: SM00065; GAF; 2.
DR SMART: SM00471; Hdc; 1.
DR PROSITE: PS00126; PDEASE_I; 1.
KW Hydrolyase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
FT LIPID 852 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 855 AA: 98797 MW: 105666 D45686D65 CRC64;

Query Match 29.6%; Score 1039.5; DB 1; Length 855;
Best Local Similarity 35.5%; Pred. No. 8.5e-62;
Matches 234; Conservative 119; Mismatches 249; Indels 57; Gaps 11;

QY 54 KDRRENDEIDKTYKTKSLCMPRSSDGETIGVAQAINKEPEAPTEDEKVMOMYL 113
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
155 KNSHESDFMDQGTGVTRNLATPIVMGK-EVLAVFMVANKV-DASESKQDEEVSXYL 212
QY 114 PFCGTAGISNAOLFASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKERC 173
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
213 SFVSIILKHLHTNYLNTESRRSQILMWSANKVPEELTDVERQPHKALYTVRTYLCERY 272
QY 174 SVLL-EDIESPVVKTKSFELMSPKCSADAENF-----KESME---KS 214
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
273 SIGLLDMTKKEFYDEWPKVGEVPEYKGPPTDGRVIFYKIIDYILHGKEEIKVPTP 332
QY 215 SYSDWLNNISAEIIVASGLPVTNISDAYQDPRFAEADQI--SGFHRSVLCVPIWNSH 272
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
333 PMDHWTLISGLPTYVAENGFFICMLNAPADEYFFQKGPVDETGWIKNVLSPVINKKE 392
QY 273 QIIGVAQVNLRLDGKPPDADQRLFAEFVFCGLGINNTIMYDQVKSWSKVALDVL 332
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
393 DIVGVATFNRKDGKPPDEYDEHIAETLTQFLGWSLLNTDTYERKNLENKRDIAQEM 452
QY 333 VHATCSKAEDV--KFK-AANIPLVSELA-----IDIHEDDFSLD 369
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
453 NHTKATPDEIKSLKFEKLEKLNIDVEDCEEKOLVTLKEDLPDPTADLYEFRRHLPT 512
QY 370 VDMATTAALRMFMELGMVQKFKIDYETLCRLMLLTVKRYRMVLYNNWRHAFNVQOLMFAM 429
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
513 EHELKGLRLFFEEINNVKEKVPVEVLTVMYTVKGYRAVTVYNNWRHGFNGVGTMTL 572
QY 430 LTTAGFQDILTEVEILAVIGCLDHRGTNNAFQAKSGSALAQLVGTSTATLEHHFN 489
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
573 LMTGLKRYTDLAEAFALAAFCCHDIDHRTNLYQMKTSPLARHG-SILLERHLE 631
QY 490 HAVMLTQSEGHNIIFANLSSKEYSDLMQLLKOSILATDLTLFERTFEFFELVSKGE--- 545
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
632 YSKLLQDESINIFQNLKRGYEVVILFVAILATDLALFYKRTMFQKIVDACEKMET 691
QY 546 -----YDWNKNIHRDIFRSMILMTACDLGAYTKPWEISROVAELVTSFEFFQGDRLREL 599
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
692 EEEAIKYVTDPTKKEIIMAMMTACDLSAITKPWEVQSVALLVANEFEGDLERTVL 751
QY 600 KLTSAIFDRNRKDELPLQLEWIDSICMPLYQALVKVNLKPMLDVATNRSKWEEL 658
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
752 QOOPIPMMDNRKDKDELPLQVGFDVCTFYVKEFSRPHKEITPMLNGLQNNRVEWKS 810

RESULT 8
CNRA_BOVIN
ID CNRA_BOVIN STANDARD; PRT; 858 AA.
AC P11541;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
DE (EC 3.1.4.17) (GMP-PDE alpha) (PDE V-B1).
GN PDE6A OR PDEA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
```

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169986; PubMed=2155175;
RA Pittler S.J., Baehr W., Wasmuth J.J., McConnell D.G., Champagne M.S.,
RA Vantuinen P., Ledbetter D., Davis R.L.;
RT "Molecular characterization of human and bovine rod photoreceptor
RT cGMP phosphodiesterase alpha-subunit and chromosomal localization of
RT the human gene.";
RL Genomics 6:272-283(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=88082056; PubMed=2826095;
RA Yu A., Ovchinnikov A., Gubanov V.V., Khrantsov N.V.,
RA Akhmedov N.B., Ischenko K.A., Zagranichnyi V.E.,
RA Vasilievskaya I.A., Rakitina T.V., Atabekova N.V., Barinov A.A.,
RA Muradov K.G., Shuvaeva T.M., Bystrov N.S., Severtsova I.V.,
RA Lipkin V.M.;
RT "Cyclic GMP phosphodiesterase from the bovine retina. Amino acid
RT sequence of the alpha-subunit and nucleotide sequence of corresponding
RT cDNA.";
RL Dokl. Akad. Nauk SSSR 296:487-491(1987).
RN [3]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=88030033; PubMed=2822478;
RA Ovchinnikov Y.A., Gubanov V.V., Khrantsov N.V., Ischenko K.A.,
RA Zagranichnyi V.E., Muradov K.G., Shuvaeva T.M., Lipkin V.M.;
RT "Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence
RT of the alpha-subunit and nucleotide sequence of the corresponding
RT cDNA.";
RL FEBS Lett. 223:169-173(1987).
CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC -----
CC EMBL; X12756; CAA31243.1; -
CC EMBL; M27541; AAA30441.1; -
CC EMBL; M36683; AAA30442.1; -
CC EMBL; M26043; AAA30443.1; -
CC PIR; S06418; S06418.
CC PIR; A34611; A34611.
CC InterPro; IPR003018; GAF.
CC InterPro; IPR003607; ME_Pplase_Hdc.
CC InterPro; IPR002073; PDEase.
CC InterPro; IPR001230; Prenyl_site.
CC Pfam; PF00233; PDEase; 1.
CC Pfam; PF01590; GAF; 2.
CC PRINTS; PR00387; PDIESTERASE1.
CC SMART; SM00065; GAF; 2.
CC SMART; SM00471; Hdc; 1.
CC PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolyase; cGMP; Vision; Prenylation; Lipoprotein; Acetylation.
FT INT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT LIPID 855 855 FARNESYL (BY SIMILARITY).
FT VARIANT 380 380 M -> V.
FT CONFLICT 193 193 V -> A (IN REF. 2 AND 3).
FT CONFLICT 423 423 T -> A (IN REF. 2 AND 3).
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FT CONFLICT 674 674 F -> C (IN REF. 2 AND 3).
SQ SEQUENCE 858 AA: 99209 MW: 86624E43662A95CC CRC64;

Query Match
Best Local Similarity 29.3%; Score 1030; DB 1; Length 858;
Matches 225; Conservative 138; Mismatches 248; Indels 80; Gaps 12;

Qy 54 KDRFNDEIDKLTGYKTKSLCMLPIRSSDGEIIGVAQAINKIPGAPTEDEKVMQYL 113
Dy 157 EDEHFCDFVDLTLEYQTKNILASPMNGK-DVVALIMVNVKV-DGPHFTEDEILLKYL 214

Qy 114 PFCGTAISNAOLFPAASRKEYERSRALLEVNDLFEEDTLEKIVKIMHRAQTLLKCRC 173
Dy 215 NFANLIMKVFHLSYLHNCETRRGQILLWSGSKVFEELTDIERQHFHALYTVRAFLNCDRY 274

Qy 174 SVLLEDESPPVVKTFKSFEL-----MSPKCSADAENSF-----KESME 212
Dy 275 SVGLLD-----MTKQKEFFDVPVLMGEAPPYAGRTPDGGEINFYKVIDYLHGKEDIK 329

Qy 213 ---KSSYSDWLINNSIAELVASTGLPVMNISDAYQDPREDAEQI---SGFHRSVLCVPI 267
Dy 330 VIPNPPDHVALVSGLPYVAQNGLICINMNAPEDEFAFOKEPLDESGWIKNVLSMPI 389

Qy 268 WNSHQIIGVAQVNLNRDGLKPFDDADQRLPFAFVIFCGLGINTIMYDQVKKSWAKOSVA 327
Dy 390 VNKEEIVGVATFYNNRDKGPFDEMDETLMESLQFLGWSVLNPDYELMKNLENRKDIF 449

Qy 328 LDVLSYHATCSKAEDV-----KPKAANIPLVSELAIDDIHFD 365
Dy 450 QDMVYHVKCDNEEIQILKTRREVYKPEWCEEBEELAEILOGELPADKYEINKHFHSD 509

Qy 366 FSLDVMAMITAAALRMFMELGMVQVKFIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVCOL 425
Dy 510 LPLTELELVKCGIQMYELKLVVDHFHQPQALVRFMYSLSGYRITYHNHRHGFNVGQT 569

Qy 426 MFAMLTAGFODIITEVILAVIVGCLDHDHGRGTNNAPFOAKSGSALQYIGSATLEH 485
Dy 570 MFSLLVTGKRYFTDLALAVMTAAAFCHDIDHRGTNNLYOMKSONPLAKLHG-SSILER 628

Qy 486 HHENHAVMILOSEGHNTFANLSKEYSDLMOLLQKOSILATDLTYLFFERTFEFFELVSKG- 544
Dy 629 HHLEFGTKLLRDESLINFONLRQKHAIHMMDIAITADLALYFKRTMQFQIVDOSK 688

Qy 545 ----EYDWN-----IKNHRDIFRSLMTACDLGAVTKPWEISROVAELVTSEFFEQGDRE 595
Dy 689 TYETQEWTOYMWLDQTRKEIVMAMMTACDLSALTTPWEVQSKVALLVAREFWEQGDLE 748

Qy 596 RLEKLTPSAIFDRNRKDELPRLOLEWIDSTCMPLYQALVKVYKLVKPLDSVATNRSKW 655
Dy 749 RTVLQONPIMPMDRNKADLPKLVGFIDFVCTFYKFEFSRFHEITPMLDGIITNNRKEW 808

Qy 656 -----EELHOKRLLASTSSSS 672
Dy 809 KALADEYETKMKGLEEKQKQQAANQAAGS 839

RESULT 9
CNRA_MOUSE
ID CNRA_MOUSE STANDARD; PRT; 858 AA.
AC P27664;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
DE (EC 3.1.4.17) (GMP-PDE alpha).
GN PDE6A OR PDEA OR MPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina.
```

```
RX MEDLINE=91130581; PubMed=18471109;
RA Baehr W., Champagne M.S., Lee A.K., Pittler S.J.;
RT "Complete cDNA sequences of mouse rod photoreceptor cGMP
RT phosphodiesterase alpha- and beta-subunits" and identification of
RT beta", a putative beta-subunit isozyme produced by alternative
RL splicing of the beta-subunit gene.";
RL FEBS Lett. 278:107-114(1991).
CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL: X60664; CAA43072.1; -
CC PIR: S13030; S13030.
CC MGD: MGI:97524; Pde6a.
CC InterPro: IPR003018; GAF.
CC InterPro: IPR003607; ME_Pplase_HDC.
CC InterPro: IPR002073; PDEase.
CC InterPro: IPR001230; Prenyl_site.
CC Pfam: PF00233; PDEase; 1.
CC Pfam: PF01590; GAF; 2.
CC PRINTS: PR00387; PDIESTERASE1.
CC SMART: SM00065; GAF; 2.
CC SMART: SM00471; HDC; 1.
CC PROSITE: PS00126; PDEASE_1; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein.
FT INIT_MET 0
FT LIPID 855 855 FARNESYL (BY SIMILARITY).
SQ SEQUENCE 858 AA: 99515 MW: E29A626B23F7DDA0 CRC64;

Query Match
Best Local Similarity 29.3%; Score 1030; DB 1; Length 858;
Matches 227; Conservative 133; Mismatches 251; Indels 80; Gaps 12;

Qy 54 KDRFNDEIDKLTGYKTKSLCMLPIRSSDGEIIGVAQAINKIPGAPTEDEKVMQYL 113
Dy 157 EDEHFCDFVDLTLEYQTKNILASPMNGK-DVVALIMAVNKIDE-PHETKRDEILLKYL 214

Qy 114 PFCGTAISNAOLFPAASRKEYERSRALLEVNDLFEEDTLEKIVKIMHRAQTLLKCRC 173
Dy 215 NFVNLIMKVFHLSYLHNCETRRGQILLWSGSKVFEELTDIERQHFHALYTVRAFLNCDRY 274

Qy 174 SVLLEDESPPVVKTFKSFEL-----MSPKCSADAENSF-----KESME 212
Dy 275 SVGLLD-----MTKQKEFFDVPVLMGEAPPYAGRTPDGGEINFYKVIDYLHGKEDIK 329

Qy 213 ---KSSYSDWLINNSIAELVASTGLPVMNISDAYQDPREDAEQI---SGFHRSVLCVPI 267
Dy 330 VIPNPPDHVALVSGLPYVAQNGLICINMNAPEDEFFFOKEPLDESGWIKNVLSMPI 389

Qy 268 WNSHQIIGVAQVNLNRDGLKPFDDADQRLPFAFVIFCGLGINTIMYDQVKKSWAKOSVA 327
Dy 390 VNKEEIVGVATFYNNRDKGPFDDMDTLMESLTQFLGWSVLNPDYTESMKNLENRKDIF 449

Qy 328 LDVLSYHATCSKAEDVDEKFAA-----NIPLVSELAIDDIHFD 365
Dy 450 QDIVKYHVKCDNEEIQILKTRREVYKPEWCEEBEELAEILOGELPADKYEINKHFHSD 509

Qy 366 FSLDVMAMITAAALRMFMELGMVQVKFIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVCOL 425
Dy 510 LPLTELELVKCGIQMYELKLVVDHFHQPQALVRFMYSLSGYRITYHNHRHGFNVGQT 569
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Db 637 YSKTLQDSNIFQNLKRFETVIHLFEVATATDLALYFKRTMFQKIVDACEQMOT 696
Qy 546 -----YDWNKIKRIDFRSLMTACDLGAVTKPWEISROVAELVSEFFEQGRERLEL 599
Db 697 EEEAIKYVTVPTKKEIIMAMMTACDLSAITKPWEVOSQVAMVAFWFEQGLERTVL 756
Qy 600 KLTSAPIDRNKDELPLQLIEWIDISCMPLYQALVKYVNVKLKPLMDSVATNRKWEEL 658
Db 757 QQQPIPMMDNRKDELPLQVGFIDFVCTFYVKEFSRPHKEITPMLSLQNNRVEWKSU 815

RESULT 11
CNRB_CANFA STANDARD: PRT: 856 AA.
AC P33726;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Rod cgmP-specific 3',5'-cyclic phosphodiesterase beta-subunit.
DE (EC 3.1.4.17) (GMP-PDE beta).
GN PDE6B OR PDEB OR PDBS.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Red setter; TISSUE=Retina;
RX MEDLINE=93249211; PubMed=8387203;
RA Suber M.L., Pittler S.J., Qin N., Wright G.C., Holcombe V.,
RA Lee R.H., Craft C.M., Lolley R.N., Baehr W.B., Hurwitz R.L.;
RT "Irish setter dogs affected with rod/cone dysplasia contain a nonsense
RT mutation in the rod cgmP phosphodiesterase beta-subunit gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:3968-3972(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Boxer X Doberman; TISSUE=Retina;
RA Clements P.J.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
CC FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- DISEASE: IRISH SETTER DOGS AFFECTED WITH ROD/CONE DYSPLASIA (RCD1)
CC CONTAIN A NONSENSE MUTATION IN THE GENE THAT GIVES RISE TO A
CC PROTEIN OF 807 AA LACKING 49 AA IN THE C-TERMINAL.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z23014; CAA80557.1;
DR EMBL; L13262; AAA30882.1; ALT_SEQ.
DR PIR; S34290; S34290.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDc.
DR InterPro; IPR002073; PDEase.
DR pfam; PF00233; PDEase; 1.
DR pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
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DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cgmP; Vision; Prenylation; Lipoprotein; Membrane;
FT Disease mutation.
FT CHAIN 1 853 ROD CGMP-SPECIFIC 3',5'-CYCLIC
FT PROPEP 854 856 PHOSPHODIESTERASE BETA-SUBUNIT.
FT LIPID 853 853 REMOVED IN MATURE FORM (BY SIMILARITY).
FT GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 856 AA; 98461 MW; AC9D03F64D1BA132 CRC64;

Query Match 29.1%; Score 1024; DB 1; Length 856;
Best Local Similarity 34.1%; Pred. No. 9.2e-61;
Matches 231; Conservative 125; Mismatches 243; Indels 78; Gaps 12;

Qy 46 LIQQTKTDRRNFDEIDKLTGYKTKSLLCMPIRSSDGEIIGVACAIINKPEGAFETDD 105
Db 148 MVNVQDVTECPHFSPFADELGTGYETRNILATPIMNGK-DVVAVIMALKL-DGCPFTSED 205
Qy 106 EKVQMOMLPFCGIAISNAQLFAASRKEYERSRALLEVVDLFEQTDLEKIVKKIMHRAQ 165
Db 206 EDVFLKYLNFGTNLKIYHLSVLHNCETRRGOVLLWSANKVFEELTDIERQPHKAFYTVR 265
Qy 166 TLLKCERCSSLLEDIESPVVKFTKSFEL-----MSPKCSADAENSF----- 207
Db 266 AYLCNDRYSGVLLD-----MTKEKEFFDVPVLMGEAQPFYSGRTPDGRREIVFYKVIDYI 320
Qy 208 ---KESME--KSSYSD-WLINNSIAELVASTGLPVPNISDAYODPRFAEADQI--SGPHI 259
Db 321 LHGKEDIKVIPSPADHWALASGLPTYVAESGFCININTRADEMFTQEGPLDDSGWVI 380
Qy 260 RSVLCVPIWNSNHQIIGVAQVLNRLDGRKPFDDADQRLFEAFVIFCGLGINTINIMYDOVKK 319
Db 381 KNVLSMPVNVKKEEIVGVATFVNRKDGKPFDEQDEVLMSLTQFLGWSVLNTDTYDKNNK 440
Qy 320 SWAKQSVALDVLVSHATCSKAEDVKEKAA-----IPLVSELA 357
Db 441 LENRKDIADQMVLYHVRCDKDEIQILPTRELRGKEPADCEDELGILLKEVLPGPSKFD 500
Qy 358 IDDTDFDQSLDQDAMITAAALRMEMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWR 417
Db 501 IYEFHFSDECTELELVKCGIQMYEVLGVVRKFIQDQEVLFVFLSVSKGYRRIYHNWR 560
Qy 418 HAFNVQQLMFAMLTATAGFDILTEVEILAVIYGCCLCHDLDRHGTNNAFQAKSGSALAQLY 477
Db 561 HGFNVAAQMTFLTTLTGKLSYYTDLFAFAMVTAGLCHDIDHRGTNNLYQMKSONPLAKLH 620
Qy 478 GTSATLEHHHFNHVMIIQSECHNIFANLSKEYSDMLQMLKQSLATDLTLTYFERRTEF 537
Db 621 G-SSILERHHLFEFGKFLSEETLNIIYQNLNRROHEVHLMDIALIATDLALYFKRTMF 679
Qy 538 FELYSKGEYDNINKNHRD-----IFRSMLMTACDLGAVTKPWEISROVA 581
Db 680 QKIVDES-----KNYEDRKSWEVYLSLETTRKELVMAAMMTACDLSAITKPWEVQSKVA 733
Qy 582 ELVTSEFFEQGRERLELKLTPSAIFDRNRKDELPLQLIEWIDISCMPLYQALVKYVNVKL 641
Db 734 LLVAAEFEWQGLDERTVLDDQPIPMMDNRKAAELPKLVQGVDFDVCFTVYKFEFSRHEEI 793
Qy 642 KPMLDVSATNRKWEEL 658
Db 794 LPMFDRLQNNRKEWKA 810

RESULT 12
CNRB_HUMAN STANDARD: PRT: 854 AA.
AC P35913; Q9BWH5;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rod cgmP-specific 3',5'-cyclic phosphodiesterase beta-subunit
DE (EC 3.1.4.17) (GMP-PDE beta).
CN PDE6B OR PDEB.
```


OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=93351644; PubMed=8394243;
 RA Khrantsov N.V., Feshchenko E.A., Suslova V.A., Shmukler B.E.,
 RA Terpigov B.E., Rakitina T.V., Atabekova N.V., Lipkin V.M.;
 RT "The human rod photoreceptor cGMP phosphodiesterase beta-subunit.
 RT Structural studies of its cDNA and gene.";
 RL FEBS Lett. 327:275-278(1993).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=93244036; PubMed=1338685;
 RA Khrantsov N.V., Feshchenko E.A., Suslova V.A., Terpigov B.E.,
 RA Rakitina T.V., Atabekova N.V., Shmukler B.E., Lipkin V.M.;
 RT "Structural studies of cDNA and the gene for the beta-subunit of cGMP
 RT phosphodiesterase from human retina.";
 RL Bioorg. Khim. 18:1551-1554(1992).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=92347868; PubMed=1322354;
 RA Collins C., Hutchinson G., Kowbel D., Weber B., Hayden M.R.;
 RT "The human beta-subunit of rod photoreceptor cGMP phosphodiesterase.";
 RT complete retinal cDNA sequence and evidence for expression in brain.";
 RL Genomics 13:698-704(1992).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=92066478; PubMed=1720239;
 RA Weber B., Riess O., Hutchinson G., Collins C., Lin B., Kowbel D.,
 RA Andrew S., Schapert K., Hayden M.R.;
 RT "Genomic organization and complete sequence of the human gene encoding
 RT the beta-subunit of the cGMP phosphodiesterase and its localisation to
 RT 4p16.3.";
 RL Nucleic Acids Res. 19:6263-6268(1991).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP SEQUENCE OF 238-854 FROM N.A.
 RC TISSUE=Retinal rod cell;
 RX MEDLINE=96330350; PubMed=8768262;
 RA Suslova V.A., Suslov O.N., Kim E.E., Lipkin V.M.;
 RT "Organization of the gene for the beta-subunit of human photoreceptor
 RT cyclic GMP phosphodiesterase.";
 RL Bioorg. Khim. 22:256-263(1996).
 RN [17]
 RP VARIANT ADPRP TYR-557.
 RX MEDLINE=93350628; PubMed=8394174;
 RA McLaughlin M.E., Sandberg M.A., Berson E.L., Dryja T.P.;
 RT "Recessive mutations in the gene encoding the beta-subunit of rod
 RT phosphodiesterase in patients with retinitis pigmentosa.";
 RL Nat. Genet. 4:130-134(1993).
 RN [18]
 RP VARIANT CSNB3 ASN-258.
 RX MEDLINE=94355978; PubMed=8075643;
 RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
 RT "Heterozygous missense mutation in the rod cGMP phosphodiesterase
 RT beta-subunit gene in autosomal dominant stationary night blindness.";
 RL Nat. Genet. 7:64-68(1994).
 RN [19]
 RP ERRATUM.
 RX MEDLINE=95038845; PubMed=7951329;
 RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
 RL Nat. Genet. 7:551-551(1994).
 RN [10]
 RP VARIANT ADPRP ASP-576.

RX MEDLINE=96129294; PubMed=8595886;
 RA Danciger M., Blaney J., Gao Y.Q., Zhao D.Y., Heckenlively J.R.,
 RA Jacobson S.G., Farber D.B.;
 RT "Mutations in the PDE6B gene in autosomal recessive retinitis
 RT pigmentosa.";
 RL Genomics 30:1-7(1995).
 RN [11]
 RP VARIANT ADPRP ARG-699.
 RX MEDLINE=96273603; PubMed=8698075;
 RA Gao Y.Q., Danciger M., Zhao D.Y., Blaney J., Piriev N.I., Shih J.,
 RA Jacobson S.G., Heckenlively J.H., Farber D.B.;
 RT "Screening of the PDE6B gene in patients with autosomal dominant
 RT retinitis pigmentosa.";
 RL Exp. Eye Res. 62:149-154(1996).
 RN [12]
 RP VARIANT ADPRP ARG-699.
 RX MEDLINE=96140746; PubMed=8557257;
 RA Valverde D., Solans T., Grinberg D., Balcells S., Vilageliu L.,
 RA Bayes M., Chivelet P., Besmond C., Goossens M., Gonzalez-Duarte R.,
 RA Baiget M.;
 RT "A novel mutation in exon 17 of the beta-subunit of rod
 RT phosphodiesterase in two RP sisters of a consanguineous family.";
 RL Hum. Genet. 97:33-38(1996).
 RN [13]
 RP VARIANT ADPRP GLN-552.
 RX MEDLINE=97114306; PubMed=8956055;
 RA Valverde D., Baiget M., Seminago R., del Rio E., Garcia-Sandoval B.,
 RA del Rio T., Bayes M., Balcells S., Martinez A., Grinberg D., Ayuso C.;
 RT "Identification of a novel R552Q mutation in exon 13 of the
 RT beta-subunit of rod phosphodiesterase gene in a Spanish family with
 RT autosomal recessive retinitis pigmentosa.";
 RL Hum. Mutat. 8:393-394(1996).
 RN [14]
 RP VARIANT ADPRP ASN-535.
 RX MEDLINE=98205225; PubMed=9543643;
 RA Saga M., Mashima Y., Akeo K., Kudoh J., Oguchi Y., Shimizu N.;
 RT "A novel homozygous Ile535Asn mutation in the rod cGMP
 RT phosphodiesterase beta-subunit gene in two brothers of a Japanese
 RT family with autosomal recessive retinitis pigmentosa.";
 RL Curr. Eye Res. 17:332-335(1998).
 CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
 CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
 CC FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
 CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2O) =
 CC guanosine 5'-phosphate.
 CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
 CC BETA). AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF RETINITIS PIGMENTOSA
 CC (RP). RP IS A GROUP OF HUMAN DISEASES THAT LEADS TO DEGENERATION
 CC OF RETINAL PHOTORECEPTOR CELLS. PATIENTS TYPICALLY HAVE NIGHT
 CC VISION BLINDNESS AND LOSS OF MIDPERIPHERAL VISUAL FIELD; AS THEIR
 CC CONDITION PROGRESSES, THEY LOOSE THEIR FAR PERIPHERAL VISUAL FIELD
 CC AND EVENTUALLY CENTRAL VISION AS WELL. RP MAY OCCUR WITH AUTOSOMAL
 CC RECESSIVE (20-25% OF CASES; ADPRP) AUTOSOMAL DOMINANT (15-20% OF
 CC CASES; ADPRP) OR X-LINKED (10-15% OF CASES; XRP) INHERITANCE.
 CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF CONGENITAL STATIONARY
 CC NIGHT BLINDNESS (CSNB3).
 CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
 CC -!- DATABASE: NAME-Mutations of the PDE6A/B/G genes;
 CC NOTE-Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/pdemut.htm".
 CC -----
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 CC -----
 CC EMBL; S41458; AAB22690.1; -

DR EMBL; X66142; CAA46932.1; -
DR EMBL; X62692; CAA44569.1; -
DR EMBL; X62693; CAA44569.1; JOINED.
DR EMBL; X62694; CAA44569.1; JOINED.
DR EMBL; X62695; CAA44569.1; JOINED.
DR EMBL; X90587; CAA62215.1; -
DR EMBL; X90588; CAA62215.1; JOINED.
DR EMBL; X90589; CAA62215.1; JOINED.
DR EMBL; X90590; CAA62215.1; JOINED.
DR EMBL; BC000249; AAH00249.1; -
DR PIR; A42828; A42828.
DR PIR; S34590; S34590.
DR Genew; HGNC:8786; PDE6B.
DR MIM; 180072; -
DR MIM; 163500; -
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane;
KW Retinitis pigmentosa; Disease mutation.
FT CHAIN 1 851 ROD CGMP-SPECIFIC 3',5'-CYCLIC
FT PROPEP 852 854 PHOSPHODIESTERASE BETA-SUBUNIT.
FT LIPID 851 851 REMOVED IN NATURE FORM (BY SIMILARITY).
FT VARIANT 74 74 GERANYL-GERANYL (BY SIMILARITY).
FT VARIANT 166 166 R -> C (IN ARRP).
FT VARIANT 212 212 E -> K (IN ARRP).
FT VARIANT 219 219 Y -> H (IN ARRP).
FT VARIANT 219 219 Y -> H (IN ARRP).
FT VARIANT 228 228 L -> H (IN ARRP AND ARRP).
FT VARIANT 228 228 L -> I.
FT VARIANT 258 258 H -> N (IN CSN83).
FT FTIG-Var_009289.
Query Match 29.0%; Score 1020; DB 1; Length 854;
Best Local Similarity 34.4%; Pred. No. 1.7e-60;
Matches 229; Conservative 118; Mismatches 240; Indels 78; Gaps 11;
QY 58 FNDEIDKLTGYTKSLCLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCG 117
D 160 FSSFADELDTYKTKMLATPINNGR-DVAVIMAYNKL-NGPFTFSEDEDFVLKLYNFAT 217
QY 118 IAINSAQLFAASRKEYSRALLEVVNDLFEBQTDLEKIVKIMHRAQTLKRCRSVLL 177
D 218 LYLKIYHLSYHNCETRRGQVLLWSANKVFELTDIERQHAFVTVRAYLLNCYRSGVL 277
QY 178 LEDIESPVVKKFKSPELMS-----PKCSADAENF-----KESME--K 213
D 278 LD-----MTKEKEFFDWSVLNGESQPSGPRTPDGRFVYKVIDYLHGKEEIKVIPT 332
QY 214 SSYSDWLNNINSAELVASTGLPVPINSDAYQDPRFDAEDQI--SGFHRSVLICVPIWNSN 271
D 333 PSADHWALASGLPSYVAESGFTICNINNASADENFKFQEGALDDSGWLKNVLSMIVNKK 392
QY 272 HQIIGVAQVNLKDGKPPDDAQRLFEAFVIFCGIINNNTIMYDQVKSWAKQSVALDYL 331
D 393 EFIGVATYVNRKDGKPPDEQDEVLMSLTQLGWSVMNTDITYDKMKNLENKDKIAQDMV 452
QY 332 SYHATCSKAEVDKFAANPIVSELA-----IDDIHDFDSDL 369

Db 453 LYHVKCDRDEIQIILPTRARLKGEPACDCEDELGEILKEELPGPTTFDIYEFHFSDLECT 512
QY 370 VDAMITAAALRMFMELCMQVKEDIDYETLCRWLLTVKRNRYMVLVYHNWRAFNVCQMFAM 429
Db 513 ELDLVKCGIOMYELGVVRKFOIPQEVLYRFLFESISKGYRITYHNWRCGFNVAQTMFTL 572
QY 430 LTTAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSALAQLYGTSTLEHHFN 489
Db 573 LMTGKLKSYTDLFAFAMVTAGLCHDIDHGTNNLYQMSQNPQAKLHG-SSILRRHLE 631
QY 490 HAVMILQSEGHNTFANLSSKEYSDLMQLLKQSLATDLTLTYFERRTEFEFELYSKGEYDWN 549
Db 632 FCKFLLSEETLIYQNLNRQHEVYIHLMDIAIIATDLALYFKKRAMFOKVIDES----- 686
QY 550 IKNHDR-----IFRSLMTACDLGAVTKPWEISROVAELVTSEFFEQGD 593
Db 687 -KNYODKKSWEVLSLETTTRKELVMAAMMTACDLSAITKPWEVQSVALLVAEFWEQGD 745
QY 594 REKLELKLTPSAIFDRNRKDELPRQLEWIDSCIMPLYQALYKVVNKKLPMLDSVATNRS 653
Db 746 LERTVLDQOPIPMMDRNKAAELPKLVGFTDFVCTFVYKEFSRHFHEILPMFDRQLNRRK 805
QY 654 KWEEL 658
Db 806 EWKAL 810
RESULT 13
CNRB_MOUSE
ID CNRB_MOUSE STANDARD; PRT; 856 AA.
AC P23440;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rod CGMP-specific 3',5'-cyclic phosphodiesterase beta-subunit
DE (EC 3.1.4.17) (GMP-PDE beta).
GN PDE6B OR PDEB OR RD OR MPB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=91015387; PubMed=1977087;
RA Bowes C., Li T., Danciger M., Baxter L.C., Applebury M.L.,
RA Farber D.B.;
RT Retinal degeneration in the rd mouse is caused by a defect in the
RL beta subunit of rod cGMP-phosphodiesterase.";
RL Nature 347:677-680(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=91130581; PubMed=1847109;
RA Baehr W., Champagne M.S., Lee A.K., Pittler S.J.;
RT "Complete cDNA sequences of mouse rod photoreceptor cGMP
phosphodiesterase alpha- and beta-subunits, and identification of
beta", a putative beta-subunit isozyme produced by alternative
RT splicing of the beta-subunit gene";
RL FEBS Lett. 278:107-114(1991).
CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
guanosine 5'-phosphate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Beta';
are produced by alternative splicing
CC -!- DISEASE: DEFECTS IN PDE6B ARE THE CAUSE OF RETINAL DEGENERATION.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY.

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:49:06 ; Search time 49.0797 Seconds
(without alignments)
1490.031 Million cell updates/sec

Title: US-09-663-542-1

Perfect score: 3516

Sequence: 1 MLKQARRPLFRNVLSTQWK.....ASTASSSSPASVMVAKEDRN 684

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3250	92.4	934	10	US-09-891-216-12
3	3250	92.4	934	10	US-09-891-216-15
4	2970	84.5	576	10	US-09-891-216-13
5	2541	72.3	490	9	US-10-094-1688-1
6	1762	50.1	367	9	US-10-094-1688-3
7	1366.5	38.9	875	9	US-10-115-515-23
8	1366.5	38.9	875	9	US-10-094-1688-5
9	1355.5	38.6	875	9	US-10-115-515-10
10	1352	38.5	833	10	US-09-891-216-3
11	956	27.2	789	10	US-09-321-801-2
12	956	27.2	791	10	US-09-321-801-4
13	950	27.0	779	10	US-09-420-190-1
14	934.5	26.6	905	12	US-10-094-989-4
15	934.5	26.6	920	12	US-10-094-989-2
16	934.5	26.6	941	10	US-09-883-825-45
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18	920.5	26.2	921	10	US-09-883-825-39
19	920.5	26.2	921	12	US-10-094-989-5

Sequence 43, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 21, Appl
Sequence 2, Appl
Sequence 17, Appl
Sequence 2, Appl
Sequence 16, Appl
Sequence 23, Appl
Sequence 47, Appl
Sequence 49, Appl
Sequence 10, Appl
Sequence 9, Appl
Sequence 51, Appl
Sequence 6, Appl
Sequence 8, Appl
Sequence 50, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 46, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-891-216-14
; Sequence 14, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973 00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 684
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-14

Query Match 100.0%; Score 3516; DB 10; Length 684;
Best Local Similarity 100.0%; Pred. No. 7.9e-297;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLKQARRPLFRNVLSTQWKVKITRLVQISGASLAEKQKHQDFLIQRTTKTKDRFND 60
Db 1 MLKQARRPLFRNVLSTQWKVKITRLVQISGASLAEKQKHQDFLIQRTTKTKDRFND 60
Qy 61 EIDLKTYKYSLLCMPISRSDGEIIGVAQAINIPEGAPTEDEKVMQYLPFCGTAI 120
Db 61 EIDLKTYKYSLLCMPISRSDGEIIGVAQAINIPEGAPTEDEKVMQYLPFCGTAI 120
Qy 121 SNAOLFAASKEYERSRALLVNDLFEQTDLEKIVKIMHRAQTLKLCERCSSLLED 180
Db 121 SNAOLFAASKEYERSRALLVNDLFEQTDLEKIVKIMHRAQTLKLCERCSSLLED 180
Qy 181 IESPVVFKTSFELMSPKCSADAENSKESKSYSDWLINNSIAELVASTGLPVD 240

181 IESPVVFTKSFELMSPKCSADAENSEPKESMEKSSYSDWLNINNSIAELVASTGLPVNISD 240
Db :|||||
Qy :|||||
241 AYQDPREDAEQISGFHRSVLCVPTWNSNHQIIGVAQVNLRLDGGKPFDDADQRLFEAF 300
Db :|||||
Qy :|||||
241 AYQDPREDAEQISGFHRSVLCVPTWNSNHQIIGVAQVNLRLDGGKPFDDADQRLFEAF 300
Db :|||||
Qy :|||||
301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLVSYHATCSKAEDVKFKAANIPLVSELAIDD 360
Db :|||||
Qy :|||||
301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLVSYHATCSKAEDVKFKAANIPLVSELAIDD 360
Db :|||||
Qy :|||||
361 IHFDPDFSLVDVDMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLYHNWRHAF 420
Db :|||||
Qy :|||||
361 IHFDPDFSLVDVDMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLYHNWRHAF 420
Db :|||||
Qy :|||||
421 NVCOLMFAMLTAGFQDILTEVELAVIVGCLCHDLDRGTNNAFQAKSGSALAOLYCTS 480
Db :|||||
Qy :|||||
421 NVCOLMFAMLTAGFQDILTEVELAVIVGCLCHDLDRGTNNAFQAKSGSALAOLYCTS 480
Db :|||||
Qy :|||||
481 ATLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKOSILATDLTLTYFERTEFEFEL 540
Db :|||||
Qy :|||||
481 ATLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKOSILATDLTLTYFERTEFEFEL 540
Db :|||||
Qy :|||||
541 VSKGEYDWNINKNHRDIERSMLMTACDLGAVTKPWEISROVAELVTSEFFEQGDRERLELK 600
Db :|||||
Qy :|||||
541 VSKGEYDWNINKNHRDIERSMLMTACDLGAVTKPWEISROVAELVTSEFFEQGDRERLELK 600
Db :|||||
Qy :|||||
601 LTPSAIFDRNRKDELPRQLQLEWIDISICMPLYQALVKNVVKLKPMLDSVATNRSKWEELHQ 660
Db :|||||
Qy :|||||
601 LTPSAIFDRNRKDELPRQLQLEWIDISICMPLYQALVKNVVKLKPMLDSVATNRSKWEELHQ 660
Db :|||||
Qy :|||||
661 KRLLASTASSSSPASVMVAKEDRN 684
Db :|||||
661 KRLLASTASSSSPASVMVAKEDRN 684

RESULT 2
US-09-891-216-12
; Sequence 12, Application us/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-12

Query Match 92.4%; Score 3250; DB 10; Length 934;
Best Local Similarity 99.8%; Pred. No. 1.6e-273;
Matches 630; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 54 KDRFNDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYL 113
Db :|||||
Qy 304 QDRFNDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYL 363
Db :|||||
Qy 114 PFCGIAISNAQLFAASRKEYRSRALLEVNDLFEETDLEKIVKIMHRAQTLLKCERC 173
Db :|||||
Qy 364 PFCGIAISNAQLFAASRKEYRSRALLEVNDLFEETDLEKIVKIMHRAQTLLKCERC 423
Db :|||||

174 SVLLEDIESPVVFTKSFELMSPKCSADAENSEPKESMEKSSYSDWLNINNSIAELVASTG 233
Db :|||||
Qy :|||||
424 SVLLEDIESPVVFTKSFELMSPKCSADAENSEPKESMEKSSYSDWLNINNSIAELVASTG 483
Db :|||||
Qy :|||||
234 LPVNISDAYODPREDAEQISGFHRSVLCVPTWNSNHQIIGVAQVNLRLDGGKPFDDAD 293
Db :|||||
Qy :|||||
484 LPVNISDAYODPREDAEQISGFHRSVLCVPTWNSNHQIIGVAQVNLRLDGGKPFDDAD 543
Db :|||||
Qy :|||||
294 QRLFEAEVIFCGLGINNTIMYDQVKKSWAKOSVALDVLVSYHATCSKAEDVKFKAANIPLV 353
Db :|||||
Qy :|||||
544 QRLFEAEVIFCGLGINNTIMYDQVKKSWAKOSVALDVLVSYHATCSKAEDVKFKAANIPLV 603
Db :|||||
Qy :|||||
354 SELAIDDIHFDDFSLVDVDMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLY 413
Db :|||||
Qy :|||||
604 SELAIDDIHFDDFSLVDVDMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLY 663
Db :|||||
Qy :|||||
414 HNRHAFNVCOLMFAMLTAGFQDILTEVELAVIVGCLCHDLDRGTNNAFQAKSGSALA 473
Db :|||||
Qy :|||||
664 HNRHAFNVCOLMFAMLTAGFQDILTEVELAVIVGCLCHDLDRGTNNAFQAKSGSALA 723
Db :|||||
Qy :|||||
474 AQLYGTSAITLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKOSILATDLTLTYFER 533
Db :|||||
Qy :|||||
724 AQLYGTSAITLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKOSILATDLTLTYFER 783
Db :|||||
Qy :|||||
534 RTEFFELVSKGEYDWNINKNHRDIERSMLMTACDLGAVTKPWEISROVAELVTSEFFEQG 593
Db :|||||
Qy :|||||
784 RTEFFELVSKGEYDWNINKNHRDIERSMLMTACDLGAVTKPWEISROVAELVTSEFFEQG 843
Db :|||||
Qy :|||||
594 RERLELKTSAIFDRNRKDELPRQLQLEWIDISICMPLYQALVKNVVKLKPMLDSVATNRS 653
Db :|||||
Qy :|||||
844 RERLELKTSAIFDRNRKDELPRQLQLEWIDISICMPLYQALVKNVVKLKPMLDSVATNRS 903
Db :|||||
Qy :|||||
654 KWHEELHOKRLLASTASSSSPASVMVAKEDRN 684
Db :|||||
Qy :|||||
904 KWHEELHOKRLLASTASSSSPASVMVAKEDRN 934

RESULT 3
US-09-891-216-15
; Sequence 15, Application us/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-15

Query Match 92.4%; Score 3250; DB 10; Length 934;
Best Local Similarity 99.8%; Pred. No. 1.6e-273;
Matches 630; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 54 KDRFNDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYL 113
Db :|||||
Qy 304 QDRFNDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYL 363
Db :|||||
Qy 114 PFCGIAISNAQLFAASRKEYRSRALLEVNDLFEETDLEKIVKIMHRAQTLLKCERC 173
Db :|||||
Qy 364 PFCGIAISNAQLFAASRKEYRSRALLEVNDLFEETDLEKIVKIMHRAQTLLKCERC 423
Db :|||||

QY 174 SVLLEDIESPVVFKTSFELMSPKCSADAENSKESMEKSSYSDWLINNSIAELVASTG 233
DB 424 SVLLEDIESPVVFKTSFELMSPKCSADAENSKESMEKSSYSDWLINNSIAELVASTG 483
QY 234 LPVNISDAYQDPREDAEADQISGFHRSVLCVPWNNSHQIIGVAQVNLRLDGPFDAD 293
DB 484 LPVNISDAYQDPREDAEADQISGFHRSVLCVPWNNSHQIIGVAQVNLRLDGPFDAD 543
QY 294 QRLFEAFVFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAANPLV 353
DB 544 QRLFEAFVFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAANPLV 603
QY 354 SELAIDDIHFDLSDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY 413
DB 604 SELAIDDIHFDLSDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY 663
QY 414 HNRHAFNVCOLMFAMLTAGFODILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSAL 473
DB 664 HNRHAFNVCOLMFAMLTAGFODILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSAL 723
QY 474 AOLYGTSATLEHHFHNHAFVMILOSEGHNIFANLSSKEYSDLMQLLKOSILATDLTYFER 533
DB 724 AOLYGTSATLEHHFHNHAFVMILOSEGHNIFANLSSKEYSDLMQLLKOSILATDLTYFER 783
QY 534 RTEFFELVSKGEYDWNINKNHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEQGD 593
DB 784 RTEFFELVSKGEYDWNINKNHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEQGD 843
QY 594 RERLEKLTPSAIFDRNRKDELPRLOLEWIDISICMPLYQALVKVNVKLPMLDSVATNRS 653
DB 844 RERLEKLTPSAIFDRNRKDELPRLOLEWIDISICMPLYQALVKVNVKLPMLDSVATNRS 903
QY 654 KWEELHOKRLLASTASSSSPASVMVAKEDRN 684
DB 904 KWEELHOKRLLASTASSSSPASVMVAKEDRN 934

RESULT 4
US-09-891-216-13
; Sequence 13, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-13

Query Match 84.5%; Score 2970; DB 10; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.7e-249;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 MQMVLPCGIAISNAQLFAASRKEYSRALLVYVNDLFEQTDLEKIVKIMHRAQTLL 168
DB 1 MQMVLPCGIAISNAQLFAASRKEYSRALLVYVNDLFEQTDLEKIVKIMHRAQTLL 60
QY 169 KCERCSVLLLEDIESPVVFKTSFELMSPKCSADAENSKESMEKSSYSDWLINNSIAEL 228
DB 169 KCERCSVLLLEDIESPVVFKTSFELMSPKCSADAENSKESMEKSSYSDWLINNSIAEL 228

DB 61 KCERCSVLLLEDIESPVVFKTSFELMSPKCSADAENSKESMEKSSYSDWLINNSIAEL 120
QY 229 VASTGLPVNISDAYQDPREDAEADQISGFHRSVLCVPWNNSHQIIGVAQVNLRLDCKP 288
DB 121 VASTGLPVNISDAYQDPREDAEADQISGFHRSVLCVPWNNSHQIIGVAQVNLRLDCKP 180
QY 289 FDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAA 348
DB 181 FDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAA 240
QY 349 NIPLVSELAIDDIHFDLSDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNY 408
DB 241 NIPLVSELAIDDIHFDLSDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNY 300
QY 409 RMVLYHNRHAFNVCOLMFAMLTAGFODILTEVEILAVIVGCLCHDLDRGTNNAFQAK 468
DB 301 RMVLYHNRHAFNVCOLMFAMLTAGFODILTEVEILAVIVGCLCHDLDRGTNNAFQAK 360
QY 469 SGSALAQLYGTSATLEHHFHNHAFVMILOSEGHNIFANLSSKEYSDLMQLLKOSILATDLT 528
DB 361 SGSALAQLYGTSATLEHHFHNHAFVMILOSEGHNIFANLSSKEYSDLMQLLKOSILATDLT 420
QY 529 LYFERTEFFELVSKGEYDWNINKNHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEF 588
DB 421 LYFERTEFFELVSKGEYDWNINKNHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEF 480
QY 589 FEQGDRELEKLTPSAIFDRNRKDELPRLOLEWIDISICMPLYQALVKVNVKLPMLDSV 648
DB 481 FEQGDRELEKLTPSAIFDRNRKDELPRLOLEWIDISICMPLYQALVKVNVKLPMLDSV 540
QY 649 ATNRKSWHEELHOKRLLASTASSSSPASVMVAKEDRN 684
DB 541 ATNRKSWHEELHOKRLLASTASSSSPASVMVAKEDRN 576

RESULT 5
US-10-094-168B-1
; Sequence 1, Application US/10094168B
; Publication No. US20030092156A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.; Harrow, Ian
; APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDRES
; FILE REFERENCE: PF-0623-2 CIP
; CURRENT APPLICATION NUMBER: US/10/094,168B
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A1
US-10-094-168B-1

Query Match 72.3%; Score 2541; DB 9; Length 490;
Best Local Similarity 100.0%; Pred. No. 2.5e-212;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 MSPKCSADAENSKESMEKSSYSDWLINNSIAELVASTGLPVNISDAYQDPREDAEQI 254
DB 1 MSPKCSADAENSKESMEKSSYSDWLINNSIAELVASTGLPVNISDAYQDPREDAEQI 60
QY 255 SGFHRSVLCVPWNNSHQIIGVAQVNLRLDCKPDDADQRLFEAFVFCGLGINNTIMY 314
DB 61 SGFHRSVLCVPWNNSHQIIGVAQVNLRLDCKPDDADQRLFEAFVFCGLGINNTIMY 120

Qy 315 DOVKKSWAKQSVLDVLSYHATCSKAEDVDFKAANIPLVSELAIDDDHFDDFSLLVDAMI 374
Db 121 DOVKKSWAKQSVLDVLSYHATCSKAEDVDFKAANIPLVSELAIDDDHFDDFSLLVDAMI 180
Qy 375 TAALRMFMELGMQVKFKIDYETLCRWLLTVRKNNRMVLYHNWRAFNVCQMLFAMLTAG 434
Db 181 TAALRMFMELGMQVKFKIDYETLCRWLLTVRKNNRMVLYHNWRAFNVCQMLFAMLTAG 240
Qy 435 FQDILTEVEILAVIVGCLCHDLHRGTNNNAFOAKSGSALAOLYGTSTLEHHHFNHAMI 494
Db 241 FQDILTEVEILAVIVGCLCHDLHRGTNNNAFOAKSGSALAOLYGTSTLEHHHFNHAMI 300
Qy 495 LQSEGHNIFANLSKEYSDMLQKSLATDLTLTYFERR 534
Db 301 LQSEGHNIFANLSKEYSDMLQKSLATDLTLTYFERR 340
Qy 534 LQSEGHNIFANLSKEYSDMLQKSLATDLTLTYFERR 554
Db 301 LQSEGHNIFANLSKEYSDMLQKSLATDLTLTYFERR 360
Qy 555 DIFRMLMTACDLGAVTKPWEISQVAVELTSEFFEOGDRERLELKLTPSAIFDRNRKDE 614
Db 361 DIFRMLMTACDLGAVTKPWEISQVAVELTSEFFEOGDRERLELKLTPSAIFDRNRKDE 420
Qy 615 LPRQLEWIDSICPLQALVKNVKKPMLDSVATNRSKWEELHOKRLLASTASSSSPA 674
Db 421 LPRQLEWIDSICPLQALVKNVKKPMLDSVATNRSKWEELHOKRLLASTASSSSPA 480
Qy 675 SVMVAKEDRN 684
Db 481 SVMVAKEDRN 490
RESULT 6
US-10-094-168B-3
; Sequence 3, Application US/10094168B
; Publication No. US20030092156A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.; Harrow, Ian
; APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PR-0623-2 CJP
; CURRENT APPLICATION NUMBER: US/10/094.168B
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A2
US-10-094-168B-3
Query Match 50.1%; Score 1762; DB 9; Length 367;
Best Local Similarity 99.4%; Pred. No. 8.1e-145;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 195 MSPKCSADAENSKESMEKSSYSDWLNINNSTAELVASTGLPVNISDAYQDPRDAEADQI 254
Db 1 MSPKCSADAENSKESMEKSSYSDWLNINNSTAELVASTGLPVNISDAYQDPRDAEADQI 60
Qy 255 SGFHRSVLCVPINWNSHQIIGVAQVLRNLDGKPFDDADQRLPFAVIFGGLGNNTIMY 314
Db 61 SGFHRSVLCVPINWNSHQIIGVAQVLRNLDGKPFDDADQRLPFAVIFGGLGNNTIMY 120
Qy 315 DOVKKSWAKQSVLDVLSYHATCSKAEDVDFKAANIPLVSELAIDDDHFDDFSLLVDAMI 374
Db 121 DOVKKSWAKQSVLDVLSYHATCSKAEDVDFKAANIPLVSELAIDDDHFDDFSLLVDAMI 180

Qy 375 TAALRMFMELGMQVKFKIDYETLCRWLLTVRKNNRMVLYHNWRAFNVCQMLFAMLTAG 434
Db 181 TAALRMFMELGMQVKFKIDYETLCRWLLTVRKNNRMVLYHNWRAFNVCQMLFAMLTAG 240
Qy 435 FQDILTEVEILAVIVGCLCHDLHRGTNNNAFOAKSGSALAOLYGTSTLEHHHFNHAMI 494
Db 241 FQDILTEVEILAVIVGCLCHDLHRGTNNNAFOAKSGSALAOLYGTSTLEHHHFNHAMI 300
Qy 495 LQSEGHNIFANLSKEYSDMLQKSLATDLTLTYFERR 534
Db 301 LQSEGHNIFANLSKEYSDMLQKSLATDLTLTYFERR 340
RESULT 7
US-10-115-515-23
; Sequence 23, Application US/10115515
; Publication No. US20030054992A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Corbin, Jackie D.
; Ferguson, Kenneth M.
; Francis, Sharron H.
; Radlecek, Ann
; Loughney, Kate
; McAllister-Lucas, Linda M.
; Sonnenburg, William K.
; Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115.515
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/599,658
; FILING DATE: 21-Jun-2000
; APPLICATION NUMBER: 09/055,584
; FILING DATE: 4-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030054992Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-115-515-23
Query Match 38.9%; Score 1366.5; DB 9; Length 875;
Best Local Similarity 43.1%; Pred. No. 7.1e-110;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;
Qy 54 KORRNFDEIDKLTGYTKSLCPIRSSDGEIIGVAQAIN-KIPEGAPFTTDEDEKVMQMY 112


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Db 247 EDPFNAEVDQITGYKTSILCMPIKHNREEVGVQAQAIN-KIPEGAPFTEDDEKDFAA 306
Qy 113 LPPCGIATISNAQLFAASRKEYERSRALLEVNDLFEEDTDLKIVKIMHRAQITLLKCE 172
Db 307 LAFGCVLHNAQLVETSLLENKRNQVLDLASLIFEEOQSLEVLKIAATAITISPMQVOK 366
Qy 173 CSVLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----ESMEKSSYSDWL----- 220
Db 367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403
Qy 221 ---INNSIAELVASTGLPVNISDAYODPRFPAEADQISGFH---IRSVLCVPIMW-SNHQ 273
Db 404 ANKINMYAOYVKNMTPELNPIDVSKDRFPWTTENTGVNQOCIRSLCTPIKNGKNK 463
Qy 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVIFCGLGGINNTIMYDOVKKSWAKOSVAL 328
Db 464 VIGVCQVYNKMEENTGVKPNRNDEQLEAFVIFCGLGGINNTIMYDOVKKSWAKOSVAL 523
Qy 329 DVLSYHATCSK---AEVDKFAANIPIVSELAIDDIHEDDFSLDVMADITAAALRMFMELG 385
Db 524 EVLSYHASAAEETRELQSLAAVVPVSAQTLLKITDPSFSDFELSDELTALCTIRMTDLN 583
Qy 386 MVQFKIDYETLCRWLLTVRNKYNM-VLYHNHRHAFNVQCLMFAMLTITAGFODILTVEI 444
Db 584 LVQNFQMKHEVLCRWILSVKKNYKNVAYHNHRHAFNTAQCMFAALKAGKIQNKLTDL 643
Qy 445 LAVIVGCLCHDLDRGTNNAFQKSGSALAOLYGTSAITLHHHFNHVMILQSEGNIFA 504
Db 644 LALLIAALSHDLDRGVNSVIQSEHPLAQLY-CHSIMEHHHFDQCLMLNSPGNQILS 702
Qy 505 NLSKEYSDMLQKQSLATDLTYLFFERTFEFFELVSKGEYDWNKKNRDIKFRSMLMTA 564
Db 703 GLSIEEYTKTLIKIQAIALATDLALYIKRGEFFELIRKNQFNLEDHPQKELFLAMLTA 762
Qy 565 CDLGAVTKPWEISROVAELVTSEPFQGDRELRLEKLTSPSAIFDRNRKDELPRLOLEWID 624
Db 763 CDLSAITKPWPQIOQRIAEVLVATEFFDQGDREKRELNIPTDLMNREKKNKIPSMQVGFID 822
Qy 625 SICMPYQALYKVNKPKMLDSVATNRSKWEEL--HOKRLIASPSSSS 672
Db 823 AICLQLYEALTHVSEDCFPLLDGCGRKNRQKQWQALAEQOEKMLINGESQQA 872
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RESULT 8

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US-10-094-168B-5
; Sequence 5, Application US/10094168B
; Publication No. US20030092156A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.; Harrow, Ian
; APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDSES
; FILE REFERENCE: PF-0623-2 CIP
; CURRENT APPLICATION NUMBER: US/10/094,168B
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20030092156A1 g3355606
US-10-094-168B-5
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Query Match 38.9%; Score 1366.5; DB 9; Length 875;
Best Local Similarity 43.1%; Pred. No. 7.1e-110;

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Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;
Qy 54 KDRFNDIDKLTGYKTKSLCMPIRSDGETLIGVQAQAIN-KIPEGAPFTEDDEKVMOMY 112
Db 247 EDPFNAEVDQITGYKTSILCMPIKHNREEVGVQAQAINKKSNGGTFTTEKDEKDFAA 306
Qy 113 LPPCGIATISNAQLFAASRKEYERSRALLEVNDLFEEDTDLKIVKIMHRAQITLLKCE 172
Db 307 LAFGCVLHNAQLVETSLLENKRNQVLDLASLIFEEOQSLEVLKIAATAITISPMQVOK 366
Qy 173 CSVLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----ESMEKSSYSDWL----- 220
Db 367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403
Qy 221 ---INNSIAELVASTGLPVNISDAYODPRFPAEADQISGFH---IRSVLCVPIMW-SNHQ 273
Db 404 ANKINMYAOYVKNMTPELNPIDVSKDRFPWTTENTGVNQOCIRSLCTPIKNGKNK 463
Qy 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVIFCGLGGINNTIMYDOVKKSWAKOSVAL 328
Db 464 VIGVCQVYNKMEENTGVKPNRNDEQLEAFVIFCGLGGINNTIMYDOVKKSWAKOSVAL 523
Qy 329 DVLSYHATCSK---AEVDKFAANIPIVSELAIDDIHEDDFSLDVMADITAAALRMFMELG 385
Db 524 EVLSYHASAAEETRELQSLAAVVPVSAQTLLKITDPSFSDFELSDELTALCTIRMTDLN 583
Qy 386 MVQFKIDYETLCRWLLTVRNKYNM-VLYHNHRHAFNVQCLMFAMLTITAGFODILTVEI 444
Db 584 LVQNFQMKHEVLCRWILSVKKNYKNVAYHNHRHAFNTAQCMFAALKAGKIQNKLTDL 643
Qy 445 LAVIVGCLCHDLDRGTNNAFQKSGSALAOLYGTSAITLHHHFNHVMILQSEGNIFA 504
Db 644 LALLIAALSHDLDRGVNSVIQSEHPLAQLY-CHSIMEHHHFDQCLMLNSPGNQILS 702
Qy 505 NLSKEYSDMLQKQSLATDLTYLFFERTFEFFELVSKGEYDWNKKNRDIKFRSMLMTA 564
Db 703 GLSIEEYTKTLIKIQAIALATDLALYIKRGEFFELIRKNQFNLEDHPQKELFLAMLTA 762
Qy 565 CDLGAVTKPWEISROVAELVTSEPFQGDRELRLEKLTSPSAIFDRNRKDELPRLOLEWID 624
Db 763 CDLSAITKPWPQIOQRIAEVLVATEFFDQGDREKRELNIPTDLMNREKKNKIPSMQVGFID 822
Qy 625 SICMPYQALYKVNKPKMLDSVATNRSKWEEL--HOKRLIASPSSSS 672
Db 823 AICLQLYEALTHVSEDCFPLLDGCGRKNRQKQWQALAEQOEKMLINGESQQA 872
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RESULT 9

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US-10-115-515-10
; Sequence 10, Application US/10115515
; Publication No. US20030054992A1
; GENERAL INFORMATION:
```

```
APPLICANT: Beavo, Joseph A.
Corbin, Jackie D.
Ferguson, Kenneth M.
Francis, Sharron H.
Kadlecek, Ann
Loughney, Kate
McAllister-Lucas, Linda M.
Sonnenburg, William K.
Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
Phosphodiesterase Materials and Methods
```

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,515
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/599,658
FILING DATE: 21-Jun-2000
APPLICATION NUMBER: 09/055,584
FILING DATE: 4-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030034992Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-115-515-10

Query Match 38.6%; Score 1355.5; DB 9; Length 875;
Best Local Similarity 42.9%; Pred. No. 6.4e-109;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;
QY 54 KDRRENDEIKLTGYKTKSLLCMPIRSSDGEIIGVAAQAIN-KIPEGAPTEDEKVMQY 112
Db 237 EDPFNAEVDQITGYKTSILCKPKHREEVGVAAQAINKSGNGGTFTEKDEKDFAY 296
QY 113 LPFCGTAISNAOLFPAASRKEYERSRALLLEVNDLFEEOTDLEKIVKIMHRAQTLLKCR 172
Db 297 LAFCGIVLHNAQLYETSILENKRNOVLDDLASLIFEEOQSLEVLKIAATISFQVOK 356
QY 173 CSQLLEDIESPVKFTKSFELMSPKCSADANSEK-----ESMEKSSYSDDL----- 220
Db 357 CTIFIVD-----DCSDSFSSVFHMECELEKS--SDTLTREH 393
QY 221 ----INNSTAELVASTGLPVPNI SDAYQDPFDAEADQISGFH---IRSVLCVPIN--SNHQ 273
Db 394 ANRINYMYAQYKNTMEPLNIPDVSKDFEPTNENMGNIQOCIRSLCTPIKKGKKN 453
QY 274 IIGVAQVNLRLDG-----KPFDDAQRLEAFVFCGLGINNTIMYDQVKKSWAKOSVAL 328
Db 454 VIGVCQVKNMEETGKVKAFNRNDEQLEAFVFCGLGIQNTQMYEAVERAMAKQMTL 513
QY 329 DYLSYHATCSK---AEVDKFAANTPLYSSELAIIDDHFDDESLVDVDMITAALRMFMELG 385
Db 514 EYLSHASAEETEELSLAAVPSAQTILKIDFSFSDLSOLETALCTIRMTDLN 573
QY 386 MVQKFKIDYETLCRWLLTVRKNYRM-VLYHNHRHAFNVCOLMFAMLTTAGFODILTEVEI 444
Db 574 LVQVQMKHEVLCKWILSVKKNYKNVAYHNHRHAFNTAQCMFAALKAGKTQKRUTDLEI 633
QY 445 LAVIVGCLCHDHRGTNNAFQKSGSALAOLYGTSTALEHHHFNHVAVMILQSEGNIFA 504
Db 634 LALLAALSHDLDRGVNNSYQIRSEHPLAQLY-CHSTMEHHFPOCLMILNPGNQILS 692
QY 505 NLSREYSDLMOLLKSLATLDLTLYFERRTEFFELVSKGEVDWIKNHRDIFRSLMTA 564
Db 693 GLSIEYKTKLIIQAILATDLALYIKRGEFFELIMKNROEDHPKELFLAMLMTA 752
QY 565 CDLGAVTKPWEISROVAELVTSFPEQGDRELEKLTSPSAIFDRNRKDELPRLOLEWID 624
Db 753 CDLSAITRPWPIQORIAELVATEFFDQGRREKELNIEPADLMNREKKNIPSMQVGFID 812

QY 625 SICMPLYQALVKVNVKLLKPMLDVATNRSKWEEL--HOKRLASTASSSS 672
Db 813 AICLQLYEALTHVSEDCFPFLDGCRRKQKQWALABQOEKTLINGESSQT 862
RESULT 10
US-09-891-216-3
; Sequence 3, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: Phosphodiesterase-Like Enzyme
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Rat
US-09-891-216-3
Query Match 38.5%; Score 1352; DB 10; Length 833;
Best Local Similarity 43.8%; Pred. No. 1.2e-108;
Matches 275; Conservative 129; Mismatches 198; Indels 26; Gaps 10;
QY 54 KDRRENDEIKLTGYKTKSLLCMPIRSSDGEIIGVAAQAIN-KIPEGAPTEDEKVMQY 112
Db 205 EDPFNAEVDQITGYKTSILCKPKHREEVGVAAQAINKSGNGGTFTEKDEKDFAY 264
QY 113 LPFCGTAISNAOLFPAASRKEYERSRALLLEVNDLFEEOTDLEKIVKIMHRAQTLLKCR 172
Db 265 LAFCGIVLHNAQLYETSILENKRNOVLDDLASLIFEEOQSLEVLKIAATISFQVOK 324
QY 173 CSQLLEDIESPVKFTKSFELMSPKCSADANSEKSMESKSSYSDDLINNSIAELVAST 232
Db 325 CTIFIVD--EDCPDSESRVQMEVEEVGKSSSEPLTREHANK-----INWYAYQVYKNT 376
QY 233 GLPVPNISDAYQDPF---DAEADQISGPHIRSVLCVPIN--SNHQIIGVAQVNLRLDG--- 286
Db 377 MEPLNIPDVTKDNREPWTNENMGHINTHCIRSLCTPIKNGKKNKVIQVGCQVKNMEET 436
QY 287 ---KPFDDAQRLEAFVFCGLGINNTIMYDQVKKSWAKOSVALDVLVSYHATCSKAEVD 343
Db 437 GKIKAFNNDQGLFLEAFVFCGLGIQNTQMYEAVERAMAKQWTVLEVLSYHASAEETR 496
QY 344 KFK-----ANIPVLSLAIDDHFDDESLVDVDMITAALRMFMELGMVOKFKIDYETLCRW 400
Db 497 ELQALAAAVPSAQTILKIDFSFSDLSOLETALCTIRMTDLNVLQNFQMKHEVLCRW 556
QY 401 LLTVKKNYRM-VLYHNHRHAFNVCOLMFAMLTTAGFODILTEVEILAVIVGCLCHDLOHR 459
Db 557 ILSVKKNYKNVAYHNHRHAFNTAQCMFAALKAGKIQNKLTDLTALLIALSHDLDR 616
QY 460 GTNNAFOAKSGSALAOLYGTSTALEHHHFNHVAVMILQSEGNIFANLSKEYSDLMOLLK 519
Db 617 GVNSYIQRSEHPLAQLY-CHSTMEHHFDOCLVNLSPGNOILSGLSIEEYKTKLIIK 675
QY 520 QSLATDITLYFERTEFFELVSKGEYDWNINKNHRDIFRSLMTACDLGAVTKPWEISRQ 579
Db 676 QAILATDLALYIKRGEFFELIRKNEFSFEDPQLOKELFLAMLMTACDLSAITKWPPIQR 735
QY 580 VAEIVTSFPEQGDRELEKLTSPSAIFDRNRKDELPRLOLEWIDISCMPLYQALVKVNV 639
Db 736 IAEIVAAEFFDQGRREKELNIEPADLMNREKKNIPSMQVGFIDAICLQLYEALTHVSE 795

Db 586 ALYSTS-TMEQHHFQTSYIIQLEGNHIFSTLSSEYEQVLEIIRKAIATDLALYFGR 644
QY 535 TEFFELVSKGEYDWNKIKNRDIFRSMMLTACDLGAVTKPWEISROVAELVTSEFEQDGR 594
Db 645 KOLEMYQTGSLNLNQSHRDVRIGLMMTACDLCSTKLPVTKLTANDIYAEFWAEGD- 703
QY 595 ERLEKLTPTSAIFDRNRKDELPRQLEWIDSTCMPLYQALVKVVKLPMLDSVATNRSK 654
Db 704 EMKLGIOPIPMMDRDKDEVPOGOLGYFNAVAICPYTTLTQILPPTPELLKACRDLNQ 763
QY 655 WEELHOKRLLASTASSSPASVMWAKED 682
Db 764 WEKVIRGEETATWISSPSVAOKAAASED 791

RESULT 13

US-09-420-190-1
; Sequence 1, Application US/09420190
; Patent No. US20020081633A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph.
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide phosphodiesterase
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-420-190-1

Query Match 27.0%; Score 950; DB 10; Length 779;
Best Local Similarity 33.4%; Pred. No. 9,3e-74;
Matches 210; Conservative 136; Mismatches 264; Indels 18; Gaps 7;
QY 55 DRRENDEIDKLTGYTKSLLCMPRISSDGEIIGVAQAINKIPEGAPFTEDEKVMQVLP 114
Db 170 DEREPRTGLESRTIQSVLGLPIVTAIGDLIGILELYRHWGKEA-FCLSHQEVATANLA 228
QY 115 FCGTAISNAQLFAASRKVEYRSALLLEVNDLFEQTDLEKIVKIMHRAOTLLKCRCS 174
Db 229 WASVAIHVOVCRGLAKOTELNDLFDLVSKTYFDNIVAIDSLLEHIMIYARNLVNADRC 288
QY 175 VLLLEDIESPVVKFTKSPFELMSPKCSADAENSFKESMEKSSYSVDWLIINNSIAELVASTGL 234
Db 289 LFQVDH-----KKNELYSDLFDIGEKEGEPVFKTKREIFSEKTAGQVARTGE 339
QY 235 PWNISDAYQDPRDAEADQISGFHRSVLCVPINNSHQIIGVAQVNLRLDGKPFDDADQ 294
Db 340 VLNPIDAYADPRFNREVLDYGYTTRNLTCMPI-VSRGSGVGVQVMWNKISGSFAFKTDE 398
QY 295 RLFEAFVFCGLGINTIMYDQVKSWAKQSVALDVLVSYHATCSKAEVDKFAANIPLVS 354
Db 399 NNFKMAFVFCALAHCANHYIRHISECIYRVTEKLSYHSICTYSEEQGLMQFTLPVRL 458
QY 355 ELAIDIDHDFDLSVDAMITAAALRMFMELGMVOKFKIDYETLCRWLLTVRKNYRMVLYH 414
Db 459 CKETELPHFD--IGPRENMWPGIFVYVMVHRSCTGSCFELEKLCRFFINSVKKNYRVPYH 515
QY 415 NWRHAFVNCQLMFAMLTITAGQDILTEVEILAVIVGCLCHLDHRTGNTNNAQKSSGALA 474
Db 516 NKKHAVTVAHQYATLQNN--HTFLTDLERKGLLIACLDLDRHGFNSNSYLQKFDHPLA 573
QY 475 QLYGTSATLEHHFNHVMILQSEGHNFANLSKEYSDMLLKQSTLATDLYFERR 534
Db 574 ALYSTS-TMEQHHFQTSYIIQLEGNHIFSTLSSEYEQVLEIIRKAIATDLALYFGR 632

QY 535 TEFFELVSKGEYDWNKIKNRDIFRSMMLTACDLGAVTKPWEISROVAELVTSEFEQDGR 594
Db 633 KOLEMYQTGSLNLNQSHRDVRIGLMMTACDLCSTKLPVTKLTANDIYAEFWAEGD- 691
QY 595 ERLEKLTPTSAIFDRNRKDELPRQLEWIDSTCMPLYQALVKVVKLPMLDSVATNRSK 654
Db 692 EMKLGIOPIPMMDRDKDEVPOGOLGYFNAVAICPYTTLTQILPPTPELLKACRDLNQ 751
QY 655 WEELHOKRLLASTASSSPASVMWAKED 682
Db 752 WEKVIRGEETATWISSPSVAOKAAASED 779

RESULT 14

US-10-094-989-4
; Sequence 4, Application US/10094989
; Patent No. US20020115179A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01063DIY
; CURRENT APPLICATION NUMBER: US/10/094,989
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/754,250
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 905
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-989-4

Query Match 26.6%; Score 934.5; DB 12; Length 905;
Best Local Similarity 33.1%; Pred. No. 2.6e-72;
Matches 212; Conservative 131; Mismatches 251; Indels 47; Gaps 12;
QY 48 QRQTKTKDRRND--EIDKLTGYTKSLLCMPI--RSSDGEIIGVAQAINKIPECAPFTE 103
Db 267 KKSQQLKDLTSEDVQOQSGMLGCLQAMLCVPEVTSRATD-QVALACAFNKL-EGDLFTD 324
QY 104 DDEKVMQMYLFCGTAISNAQLFAASRKVEYRSALLLEVNDLFEQTDLEKIVKIMHR 163
Db 325 EDEHVIOHCFTYSTVLTSLTFLAFQKQKCECQALLQVAKNLFTHLDDVSVLQEIITE 384
QY 164 AOTLLKCRCSVLLLEDIESPVVKF-----TKSPELMSPKCSADAENSFKESMEKSSYS 217
Db 385 ARNLSNAEICSVFLLDQNELVAKVDFGVGDDESEYERIP----- 424
QY 218 DWLINNSTAELVASTGLPVNISDAYQDPRDAEADQISGFHRSVLCVPINNSHQIIGV 277
Db 425 ---ADQGIAGHVAATGQILNIPDAYHPLFYRGVDDSTGFRNLFCPIKKNQEVIGV 481
QY 278 AQVNLRLDGKPFDDADQRLFEAFVFCGLGINTIMYDQVKSWAKQSVALDVLVSYHATC 337
Db 482 AELVYKINGPWFSEFDEDLATAFSTYCGISTAHSLLYKKVNEAQYRSHLANEMMYHMKV 541
QY 338 SKAEVDKFAANIPLVSELAIDDIHFDIF-----SLOVDAMITAAALRMFMELGMVOKFKI 392
Db 542 SDDEYTKLLHDIQPVAAI---DSNFASFTVTPRSLPEDDTSMAILSLMQDMNFNNYKI 598
QY 393 DYETLCRWLLTVRKNYRMVLYHNRHAFNVCQLMFAMLTITAGFODILTEVEILAVIVCL 452
Db 599 DCPTLARFCLMVKGYRDPPIYNNMHAFSVSHFCYLLYKKNELNYLIEDIEIFALFISCM 658
QY 453 CHDLDRGTNNNAQKSSGALAQLYGT--SATLEHHFNHVMILQSEGHNFANLSKEY 511
Db 659 CHDLDRGTNNNSFQVASKSVLAALYSBGSVMRHHFAQATAILNTHCGNIFDHFESRKY 718
QY 512 SDLMOLKQSTLATDLYFERRTEFFELVSKGEYDWNKIKNRDIFRSMMLTACDLGAVT 571

Db 719 QRMLDLMDRIITLATDLAHLRIKFDLQKMAEVG-YDRNNKQHRLCLLMTSCDLSDDT 777
Qy 572 KPWEISROVAELVTSEFFEQDRELERLELKLTPSAIFDRNRKDELPRQLQLEWIDSICMPLY 631
Db 778 KGWKTTRKIAELIYKEFFSOGDLEK-AMGNRPWEMMDR-EKAYIPELOISFMEHIAMPIY 835
Qy 632 QALVKVNVKLPMLDSVATNRSKWEELHOKRLLASTASSSS 672
Db 836 KLLQDLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNS 876

RESULT 15

US-10-094-989-2
; Sequence 2, Application US/10094989
; Patent No. US20020115179A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063DIV
; CURRENT APPLICATION NUMBER: US/10/094,989
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/754,250
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-989-2

Query Match 26.68; Score 934.5; DB 12; Length 920;
Best Local Similarity 33.18; Pred. No. 2.7e-72;
Matches 212; Conservative 131; Mismatches 251; Indels 47; Gaps 12;
Qy 48 QROTQTKDRRND--EIDKLTGYTKTKSLLCMPI--RSSDGEIIGVQAQAINKIPIEGAPFTE 103
Db 282 KKSITQLKDLTSEDVQQLQGLMGLCQMLCPVISRATD-QVVALACAFNKL-EGDLFTD 339
Qy 104 DDEKVMQMYLPFGIAISNAQLFAASRKEYERALLVYNDLFEEQTDLEKIVKKIMHR 163
Db 340 EDEHVIQHCFHYTSTLTSTLTFQKQKCEQALQVAKNLFTHLDDVSVLLQEIITE 399
Qy 164 AOTLLKCCERSVLLLEDIESPVVKF-----TKSFELMSPKCSADAENSPKESKSSYS 217
Db 400 ARNLSNAEICSFLLDQNELVAKVFDGVDGVDDESYEIRIP----- 439
Qy 218 DWLINNSIAELVSTGLFVNISDAYODPRFDAEADQISGFHRSVLCVPIWNSNHQIIGV 277
Db 440 ---ADQGIAGHVATTGQILNPDAYAHPFLYRGVDDSTGFTRNLCFPKINENQEVIGV 496
Qy 278 AQVLRNLDGKPFDDADQRLFEAFVIFCGLGINTIMTDQVKKSWAKOSVALDVLVSYHATC 337
Db 497 AELVKNKINGPWFSEFDEDLATAFSIYGISIAHSLLYKKVNEAQYRSHLANEMMYHMKV 556
Qy 338 SKAEVDKFAANIPLVSELAIDDDIHEDDF-----SLDQDAMITAAALRMFMELGMVQKFKI 392
Db 557 SDDIYTKLLHDGIQPVAAI---DSNFASFYTPRSLPEDDTSMAILSMLQDMFNINNYKI 613
Qy 393 DYETLCRWLLTVRKRYRMVLYHNWRHAFNVQCLMFAMLTATTAGFQDILTEVEILAVIVGCL 452
Db 614 DCPFLARFCLMVKGYRDPYPHNHMAFSVSHFCYLLYKNELTNYLEDIEIFALFISCM 673
Qy 453 CHDLDRGTNNAFQAKSGSALAQLYGT-SATLEHHHFNHVMILQSEGHNFANLSKEY 511
Db 674 CHDLDRGTNNFSQVASKSVLAALYSSEGSVMERHFEAQATAILNTHGCNIFDHFSRKDY 733
Qy 512 SMLMOLLKQSTLATDLYFERRTEFFELVSKGYDMNKNHRDIFRSMMLTACDLCGAVT 571
Db 734 QRMLDLMDRIITLATDLAHLRIKFDLQKMAEVG-YDRNNKQHRLCLLMTSCDLSDDT 792

Qy 572 KPWEISROVAELVTSEFFEQDRELERLELKLTPSAIFDRNRKDELPRQLQLEWIDSICMPLY 631
Db 793 KGWKTTRKIAELIYKEFFSOGDLEK-AMGNRPWEMMDR-EKAYIPELOISFMEHIAMPIY 850
Qy 632 QALVKVNVKLPMLDSVATNRSKWEELHOKRLLASTASSSS 672
Db 851 KLLQDLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNS 891
Search completed: June 13, 2003, 15:59:21
Job time : 52.0797 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2003, 15:46:07 ; Search time 19.4761 Seconds
(without alignments)
1033.333 Million cell updates/sec

Title: US-09-663-542-1

Perfect score: 3516

Sequence: 1 MLKOARRPLRNLVLSATQW.....ASTASSSSPASMVAKEDRN 684

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCITUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2541	72.3	490	3	US-09-226-741-1
2	2541	72.3	490	4	US-09-595-514-1
3	1762	50.1	367	3	US-09-226-741-3
4	1762	50.1	367	4	US-09-595-514-3
5	1366.5	38.9	875	1	US-08-480-547A-23
6	1366.5	38.9	875	1	US-08-250-847B-23
7	1366.5	38.9	875	2	US-08-463-949A-23
8	1366.5	38.9	875	3	US-08-464-410A-23
9	1366.5	38.9	875	3	US-09-226-741-5
10	1366.5	38.9	875	4	US-09-595-514-5
11	1366.5	38.9	875	5	PCT-US94-06066-23
12	1355.5	38.6	875	1	US-08-480-547A-10
13	1355.5	38.6	875	1	US-08-250-847B-10
14	1355.5	38.6	875	2	US-08-463-949A-10
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16	1349.5	38.4	875	5	PCT-US94-06066-10
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18	951	27.0	766	4	US-09-174-437-2
19	951	27.0	803	2	US-08-951-648-4
20	951	27.0	803	4	US-09-174-437-4
21	950	27.0	779	2	US-08-951-648-6
22	950	27.0	779	4	US-09-174-437-6
23	934.5	26.6	905	4	US-09-754-250-4
24	934.5	26.6	920	4	US-07-754-250-2
25	934.5	26.6	941	1	US-07-872-644-45
26	934.5	26.6	941	1	US-08-297-494-45
27	934.5	26.6	941	1	US-08-297-510-45

28	934.5	26.6	941	1	US-08-479-532-45	Sequence 45, Appl
29	934.5	26.6	941	1	US-08-455-526-45	Sequence 45, Appl
30	934.5	26.6	941	1	US-08-455-525-45	Sequence 45, Appl
31	934.5	26.6	941	3	US-09-139-491-45	Sequence 45, Appl
32	934.5	26.6	941	5	PCT-US92-03222-45	Sequence 45, Appl
33	920.5	26.2	921	1	US-07-872-644-39	Sequence 39, Appl
34	920.5	26.2	921	1	US-08-297-494-39	Sequence 39, Appl
35	920.5	26.2	921	1	US-08-297-510-39	Sequence 39, Appl
36	920.5	26.2	921	1	US-08-479-532-39	Sequence 39, Appl
37	920.5	26.2	921	1	US-08-455-526-39	Sequence 39, Appl
38	920.5	26.2	921	1	US-08-455-525-39	Sequence 39, Appl
39	920.5	26.2	921	3	US-09-139-491-39	Sequence 39, Appl
40	920.5	26.2	921	4	US-09-754-250-5	Sequence 5, Appl
41	920.5	26.2	921	5	PCT-US92-03222-39	Sequence 39, Appl
42	920.5	26.2	942	1	US-07-872-644-43	Sequence 43, Appl
43	920.5	26.2	942	1	US-08-297-494-43	Sequence 43, Appl
44	920.5	26.2	942	1	US-08-297-510-43	Sequence 43, Appl
45	920.5	26.2	942	1	US-08-479-532-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1

US-09-226-741-1

; Sequence 1, Application US/09226741

; Patent No. 6100037

; GENERAL INFORMATION:

; APPLICANT: Phillips, Stephen C.

; APPLICANT: Lanfear, Jerry

; APPLICANT: Fawcett, Lindsay

; APPLICANT: Bandman, Olga

; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES

; FILE REFERENCE: PF-0623 US

; CURRENT APPLICATION NUMBER: US/09/226,741

; CURRENT FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 490

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

; FEATURE:

; OTHER INFORMATION: HSPDE10A1

US-09-226-741-1

Query Match	72.3%	Score 2541;	DB 3;	Length 490;
Best Local Similarity	100.0%;	Pred. No. 3.2e-231;		
Matches 490;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	195	MSPKCSADAENSFKESMEKSSYSDWLINNSTIAELVASTGLPVNISDAYQDPRFDAEAOI	254	
Db	1	MSPKCSADAENSFKESMEKSSYSDWLINNSTIAELVASTGLPVNISDAYQDPRFDAEAOI	60	
Qy	255	SGFHRSVLCVPIMNSHQIIGVAQVNLRLDCKPDDADQRLFEAFVIFCGLGINTIMY	314	
Db	61	SGFHRSVLCVPIMNSHQIIGVAQVNLRLDCKPDDADQRLFEAFVIFCGLGINTIMY	120	
Qy	315	DOVKSKWAKQSVALDVLVSHATCSKAEDVKFKAANIPLVSELAIDDIHFDDFSLOVDAMI	374	
Db	121	DOVKSKWAKQSVALDVLVSHATCSKAEDVKFKAANIPLVSELAIDDIHFDDFSLOVDAMI	180	
Qy	375	TAALRMFMELGMVQKFKDIYETLCRWLLTVRKNYRMVLYHNHRHAFNVQCLMFMALTTAG	434	
Db	181	TAALRMFMELGMVQKFKDIYETLCRWLLTVRKNYRMVLYHNHRHAFNVQCLMFMALTTAG	240	
Qy	435	FODILTEVEILAVIVGCLCHDLDRGTNNAFQKSGSALAQLYGTSTATLEHHHFHNAVMI	494	
Db	241	FODILTEVEILAVIVGCLCHDLDRGTNNAFQKSGSALAQLYGTSTATLEHHHFHNAVMI	300	
Qy	495	LOSEGHNIFANLSKEYSDLMQLLKQSLATLTLYFFERTFEFFELVSKGEYDWNINKHR	554	
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QY 555 DIFRSLMTACDLGAVTKPWEISRQVAELVTSEFFEQDRELRLEKLTPTSAIFDRNRKDE 614
DB 361 DIFRSLMTACDLGAVTKPWEISRQVAELVTSEFFEQDRELRLEKLTPTSAIFDRNRKDE 420
QY 615 LPRQLEWIDSTCMPLYQALYKVNKVKLPMLDSVATNRSKWEEHQKRLLASTASSSSPA 674
DB 421 LPRQLEWIDSTCMPLYQALYKVNKVKLPMLDSVATNRSKWEEHQKRLLASTASSSSPA 480
QY 675 SVMVAKEDRN 684
DB 481 SVMVAKEDRN 490
RESULT 2
US-09-595-514-1
; Sequence 1, Application US/09595514
; Patent No. 6416991
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-1 CIP
; CURRENT APPLICATION NUMBER: US/09/595,514
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 490
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDEL0A1
US-09-595-514-1

Query Match 72.3%; Score 2541; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 3.2e-231; Mismatches 0; Indels 0; Gaps 0;
Matches 490; Conservative 0;
QY 195 MSPKCSADAENSFKESMEKSSYSDWLNNNSIAELVASTGLPVPNISDAYQDPRFDAEADQI 254
DB 1 MSPKCSADAENSFKESMEKSSYSDWLNNNSIAELVASTGLPVPNISDAYQDPRFDAEADQI 60
QY 255 SGFHRSVLCVPINNSNHQIIGVAQVLRDLGKPFDDADQRLFEAFVIFCGLGINTIMY 314
DB 61 SGFHRSVLCVPINNSNHQIIGVAQVLRDLGKPFDDADQRLFEAFVIFCGLGINTIMY 120
QY 315 DOVKKSAQSVLDVLSYHATCSKAEDVKFAANIPLVSELAIDDIHFDDFSLOVDAMI 374
DB 121 DOVKKSAQSVLDVLSYHATCSKAEDVKFAANIPLVSELAIDDIHFDDFSLOVDAMI 180
QY 375 TAALRMFMELGMVKQFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQCLMFAMLTAG 434
DB 181 TAALRMFMELGMVKQFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQCLMFAMLTAG 240
QY 435 FQDILTEVEILAVIGCLCHDLHRGTNNAFQAKSGSALAOLYGTSALEHHHFNHAYMI 494
DB 241 FQDILTEVEILAVIGCLCHDLHRGTNNAFQAKSGSALAOLYGTSALEHHHFNHAYMI 300
QY 495 LOSEGHNIFANLSKEYSDMLQKSLATDLTYFERRTEFFELYSKGYDWNKINHR 554
DB 301 LOSEGHNIFANLSKEYSDMLQKSLATDLTYFERRTEFFELYSKGYDWNKINHR 360
QY 555 DIFRSLMTACDLGAVTKPWEISRQVAELVTSEFFEQDRELRLEKLTPTSAIFDRNRKDE 614
DB 361 DIFRSLMTACDLGAVTKPWEISRQVAELVTSEFFEQDRELRLEKLTPTSAIFDRNRKDE 420
QY 615 LPRQLEWIDSTCMPLYQALYKVNKVKLPMLDSVATNRSKWEEHQKRLLASTASSSSPA 674
DB 421 LPRQLEWIDSTCMPLYQALYKVNKVKLPMLDSVATNRSKWEEHQKRLLASTASSSSPA 480

QY 675 SVMVAKEDRN 684
DB 481 SVMVAKEDRN 490
RESULT 3
US-09-226-741-3
; Sequence 3, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 367
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: HSPDEL0A2
US-09-226-741-3
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Best Local Similarity 99.4%; Pred. No. 6.4e-158;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MSPKCSADAENSFKESMEKSSYSDWLNNNSIAELVASTGLPVPNISDAYQDPRFDAEADQI 60
QY 255 SGFHRSVLCVPINNSNHQIIGVAQVLRDLGKPFDDADQRLFEAFVIFCGLGINTIMY 314
DB 61 SGFHRSVLCVPINNSNHQIIGVAQVLRDLGKPFDDADQRLFEAFVIFCGLGINTIMY 120
QY 315 DOVKKSAQSVLDVLSYHATCSKAEDVKFAANIPLVSELAIDDIHFDDFSLOVDAMI 374
DB 121 DOVKKSAQSVLDVLSYHATCSKAEDVKFAANIPLVSELAIDDIHFDDFSLOVDAMI 180
QY 375 TAALRMFMELGMVKQFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQCLMFAMLTAG 434
DB 181 TAALRMFMELGMVKQFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQCLMFAMLTAG 240
QY 435 FQDILTEVEILAVIGCLCHDLHRGTNNAFQAKSGSALAOLYGTSALEHHHFNHAYMI 494
DB 241 FQDILTEVEILAVIGCLCHDLHRGTNNAFQAKSGSALAOLYGTSALEHHHFNHAYMI 300
QY 495 LOSEGHNIFANLSKEYSDMLQKSLATDLTYFERR 534
DB 301 LOSEGHNIFANLSKEYSDMLQKSLATDLTYFEEK 340
RESULT 4
US-09-595-514-3
; Sequence 3, Application US/09595514
; Patent No. 6416991
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-1 CIP
; CURRENT APPLICATION NUMBER: US/09/595,514
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/226,741
; PRIOR FILING DATE: 1999-01-07


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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 367
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDEL0A2
US-09-595-514-3
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Query Match 50.1%; Score 1762; DB 4; Length 367;
Best Local Similarity 99.4%; Pred. No. 6.4e-158;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 195 MSPKCSADAENSKESMEKSSYSDDLNNNSIAELVASTGLPNNISDAYODPRDFAADQI 254
Db 1 MSPKCSADAENSKESMEKSSYSDDLNNNSIAELVASTGLPNNISDAYODPRDFAADQI 60

QY 255 SGFHRSVLCVPWNHNSHQIIGVAQVNLRLDGPDDADQORLEAFVFCGLGINNTIMY 314
Db 61 SGFHRSVLCVPWNHNSHQIIGVAQVNLRLDGPDDADQORLEAFVFCGLGINNTIMY 120

QY 315 DQVKKSWAKQSVALDVLVSHATCSKAEDVKFKAANIPLYSELAIDDIHFDDESLDVMAMI 374
Db 121 DQVKKSWAKQSVALDVLVSHATCSKAEDVKFKAANIPLYSELAIDDIHFDDESLDVMAMI 180

QY 375 TAALRMFMELGMVQKFKIDYETLCRWLLTVRKNNYRMVLYHNWRAFNVCQMFAMLTAG 434
Db 181 TAALRMFMELGMVQKFKIDYETLCRWLLTVRKNNYRMVLYHNWRAFNVCQMFAMLTAG 240

QY 435 FQDILTEVELAVIVGCLCHDLDRGTNNNAFAQKSGSALAQLYGTSTATLEHHHFNHAYMI 494
Db 241 FQDILTEVELAVIVGCLCHDLDRGTNNNAFAQKSGSALAQLYGTSTATLEHHHFNHAYMI 300

QY 495 LQSEGHNIFANLSSKEYSDLMQLLKOSILATDLTLVFEER 534
Db 301 LQSEGHNIFANLSSKEYSDLMQLLKOSILATDLTLVFEER 340
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RESULT 5

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US-08-480-547A-23
; Sequence 23, Application US/08480547A
; Patent No. 5652131
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecck, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,547A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565213land, Greta E.
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; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32791
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-547A-23
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Query Match 38.9%; Score 1366.5; DB 1; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;

QY 54 KDRFNDKIDKLTGYTKSLCMLPIRSSGDEIIGVAAQAIN-KIPEGAPFTEDDEKVMQMY 112
Db 247 EDPRFNAEVDQITGYTKQSILCPKIKNHREVVGVAAINKKSGNGGTFTEKDEKFAAY 306

QY 113 LPECGTAISNAOLFPAASRKEYERSRALLEVNDLFEQTDLEKTVKKIMHRAOTLLKCR 172
Db 307 LAFCGIVLHNAQLEYTSLLENKKNQVLLDLASLIFEQQSLEVLTKIAATITISFMVOVK 366

QY 173 CSQLLEDIESPVVKETKSPFELMSPKCSADAENSFK-----ESMEKSSYSDWL----- 220
Db 367 CTIFIVDE-----DCSFSFVFHMECELEKS--SDTLTREHD 403

QY 221 ---INNSIAELVASTGLPNNISDAYODPRDFAADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 404 ANKINMYAQYVKNTMEPLNIPDYSKDKRPPTTENTGNVNNQOCIRSLCTPIKNGKKK 463

QY 274 IIGVAQVNLRLDG-----KPFDDADQORLEAFVFCGLGINNTIMYDQVKKSWAKQSV 328
Db 464 VIGVQVNLKMEENTGKVPFNNDQFLEAFVFCGLGINNTIMYDQVKKSWAKQSV 523

QY 329 DVLSYHATCSK---AEVDKFAANIPLYSELAIDDIHFDDESLDVMAMITAAALRMFELG 385
Db 524 EVLSYHASAAEETRELOSAAAQVPSAQTLKITDFSDFSELSOLETALCTIRMFDTLN 583

QY 386 MVQKFKIDYETLCRWLLTVRKNNYRM-VLYHNWRAFNVCQMFAMLTAGFDILTEVEI 444
Db 584 LVQNFQMKHEVLCRWLLSVKKNYRKNNVAYHNWRAFNVCQMFAMLTAGFDILTEVEI 643

QY 445 LAVIVGCLCHDLDRGTNNNAFAQKSGSALAQLYGTSTATLEHHHFNHAVMILOSEGHNIFA 504
Db 644 LALLIAALSHDLDRGTNNNAFAQKSGSALAQLYGTSTATLEHHHFNHAVMILOSEGHNIFA 702

QY 505 NLSKEYSDLMQLLKOSILATDLTLVPERTEFFELVSKGEYDNKNNHRRDIFRSLMLTA 564
Db 703 GLSIEEVKTKTIKQAILATDLALYIKRGEFFELIRKQNFULEDPHQLFLFAMLTMA 762

QY 565 CDLGAVTKPWEISROVAELVTSFEQDGRERLEKLKTPSAIFDRNKKDELPRQLQLEWID 624
Db 763 CDLSAITKPWPIQOIAELVATEFFDQGRERLEKLKTPSAIFDRNKKDELPRQLQLEWID 822

QY 625 SICMPYQALVKVNVKLPMLDSVATNRSKWEEL--HOKRLLASTASSSS 672
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RESULT 6

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US-08-250-847B-23
; Sequence 23, Application US/08250847B
; Patent No. 5702936
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecck, Ann
```

```

APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,847B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5702936and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-250-847B-23

Query Match 38.9%; Score 1366.5; DB 1; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;

QY 54 KDRRENDEIKLTGYKTKSLCLMPTRSSDGEIIGVQAQAIN-KIPGAPFTDEDEKVMQMY 112
DB 247 EDPRENAEVDQITGYKTOSILCMPIKNHREYVGVQAQAINKKSGNGGTFTEKDEKFAAY 306
QY 113 LPFCGIAISNAQLFAASKEYERSRALLEVVDLFEQTDLEKIVKIMHRAQTLLKCR 172
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DB 367 CRTIFVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403
QY 221 ---INNSTAELVASTGLPWNISDAYQDPFRDAEQISGFH---IRSVLCVPINW-SNHQ 273
DB 404 ANKINMYAQYVNTMEPLNDVSKDRFPWTTENTGNVQOCIRSLCTPIKNGKKNK 463
QY 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVFCGLGINNTIMYDOVKKSWAKQSVAL 328
DB 464 VIGVCQLVNKMEENTGKVKPFNRNDEQFLAEVFCGLGIQNTQMYEAVRAMAKOMTLL 523
QY 329 DVLSYHATCSK---AEVDKFKAAINPLVSELAIDDIHDFDLSLDVDMITAALRMFMELG 385
DB 524 EVLSYHASAAEETRELQSLAAAVVPSAQTLLKITDSEFSDPELSDLCTALCTIRMTDLN 583
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DB 584 LVONFOMKHEVLVILSKYKKNYRNKRNVAHNHRAFNAAOCMAKAGKIQNKLTDLLEI 643

QY 445 LAVIVGCLCHDLHRCNTNNAFOAKSGSALAQLYGTSATLEHHHFNHVAHVILQSEGHNIFA 504
DB 644 LALLIAALSHDLHRCNVNNSYTORSEHPLAQY-CHSIMEHHHFDQCLMLNSPGNQILS 702
QY 505 NLSKEYSDLMQLLKQSILATDLTLYFFERTFEFFELVSKGYDWNLIKNRHIDFRSMLMTA 564
DB 703 GLSIEYKTKLIIKQAILATDLALYIKRGEFFELIRKNQNFLEDPHQKELFLAMLMTA 762
QY 565 CDLGAVTKPWEISRQVAELVTSFEFFEQDRELEKLTPSAITPDRNRKDELPRQLWEID 624
DB 763 CDLSAITKPWIPQORIAELVATEFFDQGRERKELNIEPTDLNREKKNKIPSMQVGFID 822
QY 625 SICMPLYQALVKVNVKLPMLDSVATNRSKWEEL--HOKRLLASTASSSS 672
DB 823 AICLQLYEALTHVSEDCFPLLDGCRRKNROKQWALAEQQEKMLJNGESGGA 872

RESULT 7
US-08-463-949A-23
Sequence 23, Application US/08463949A
Patent No. 595583
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Corbin, Jackie D.
APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 595583and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-949A-23

Query Match 38.9%; Score 1366.5; DB 2; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;
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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464.410A
: FILING DATE: June 5, 1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 6037119and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/32705
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 875 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-464-410A-23

Query Match 38.9%; Score 1366.5; DB 3; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;

Qy 54 KDRFDEIDKLTGYKTKSLCMLPSSDGEIIGVQAQAIN-KIPGAPFTEDEKVMQY 112
Db 247 EDPFNAEVDGITGYKTSILCMPIKNHREVVGVGAINKKSGNGGTFTEKEDKFAAY 306
Qy 113 LPFCGIAISNAQLFAASRKEYERSRALLLEVNVNDLFEEQTDLEKIVKKIMHRAQTLLKCFR 172
Db 307 LAFCGVLVHNAQLYETSLLENKRNQVLLDLASLIFEEOQSLEVLKKAATAIISPMQVK 366
Qy 173 CSVLLIEDIESPVVKTKSFELMSPKCSADAENSPK-----ESMEKSSYSDWL----- 220
Db 367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403
Qy 221 ---TNNSTAEIIVASTGLPVNITSDAYODPFDAEADQISGFH---TRSVLCVPIWN-SNHQ 273
Db 404 ANKINMYAQVKNMTEPLNIPDVSKDRFPWTTENTGNVNOQCIRSLTCTPIKNGKKNK 463
Qy 274 IIGVAQLNRLDG-----KPEDDADQRLEAFVIFCGLGINNTIMYDQVKKSWAKQSVAL 328
Db 464 VIGVQQLVNKMEENTGKVKPENRNDQEQLEAFVIFCGLGIQNTQMYEAVERAMAKQMVTL 523
Qy 329 DVLSYHATCSK---AEVDKPKAAANTPLVSELAIDDIHFDDDSLDVDMITAALRPFMELG 385
Db 524 EVLSYHASAAEETREIQSLAAAVVPSAQTUKITDFSFDSFELSDELTALCTIRMFDTLN 583
Qy 386 MVQFKFDIYELCRWLLTVTRNRYM-VLYHNHRIAFNVCMQLFAMLTAGFODILTEVEI 444
Db 584 LVQNFQMKHEVLCRWILSVKKNRYKNVAYHNHRAFNQACMFALKACKIQNKLTDLLEI 643
Qy 445 LAVTVGCLCHDLDRGTNNFAQKSGSALAOLYGTYSATLEHHHFFHNAVMILOSEGHNIPA 504
Db 644 LALLIAALSHDLDRGVNNYSYIQRSEHPLAQLY-CHSIMEHHFFDOCLMLNSPQNQLS 702
Qy 505 NLSKEYSDLMQLLKQSTLATDLTLVFPRRTEFFELVSKGYEWNINKHRDIFRMLMTA 564
Db 703 GLSIEEYKTKUIIKQAILATDLALYIKRGEFFELIKRNFQNLDEDPHOKELFLAMLMTA 762
Qy 565 CDLGAVTKPWEISROQVALVTSFEQDGRERLELKTPSAIFDRNRKDELPRLEWID 624
Db 763 CDLSAITKWPFIQRIAEIVATEFDDQGRKERKELNIPTDLNMNREKKNKIPSMQVGFID 822
Qy 625 SICMPLVQALVKVNVKPKMLDLSVATNRSKWHEEL--HOKRLLASTASSSS 672
Db 823 AICQLQLEALPHVSDCFPLPDGCRKNRQKQWALAEQQEKMLINGESGQA 872

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RESULT 9
US-09-22


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; Sequence 23, Application PC/TUS9406066
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Washington
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ATTORNEY/AGENT INFORMATION:
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,051
; FILING DATE: 27-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32083
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-06066-23

Query Match 38.9%; Score 1366.5; DB 5; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;

QY 54 KDRFNDEIDKLTGYKTSLLCMPTRSSDGLIIGVQAQAIN-KIPGAPFTDEDEKVMQY 112
Db 247 EDPRNAEVDQITGYKTSILCMPIKNHREEVGVQAQAINKSGNGGTFTEKDKFAAY 306

QY 113 LPFCGIAISNAQLFAASRKEYERSRALLEVNDLPFEQTDLEKIVKIMHRAQTLKCEK 172
Db 307 LAFCGIVLHNAQLYETSLLENKRNQVLLDASLIFEEOQSLEVLKKAATIIISPMQVK 366

QY 173 CSVLLEDIESPVVFKTSFELMSPKCSADAENSPK-----ESMEKSSYSDDL----- 220
Db 367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403

QY 221 ---INNSTAELVASTGLPVNISDAVDPRFAEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 404 ANKINMYAQVKNMTPELNPIDVSKDRFPMTTENTGNVQOCIRSLCTPIKNGKNK 463

QY 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKSWAKOSVAL 328
Db 464 VIGVCQLYKNMEENTGKVKPNRNDEQLEAFVIFCGLGIQNTQMYEAVRAMAKQWTL 523

QY 329 DVLVSHATCSK---AEDVKFAANITPLVSELAIDDIHEDFSLDQVDMITAAALRMFELG 385
Db 524 EVLSVHASAAEETRELQSLAAAVVPSAQTLLKITDFSPDLSLELTALCTIRMTDLN 583

QY 386 MVQEKIDYETLCRWLLTVKRNRM-VLYHNHRHAFNVQCLMFAMLTITAGQDILTEVEI 444
Db 584 LVQNFQMKHEVLCKWILSVKKNRYNVAIHNHRHAFNTAQCMFALAKGAKIGKLTDL 643

; Sequence 23, Application PC/TUS9406066
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Washington
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ATTORNEY/AGENT INFORMATION:
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,051
; FILING DATE: 27-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32083
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-06066-23

Query Match 38.6%; Score 1355.5; DB 1; Length 875;
Best Local Similarity 42.9%; Pred. No. 6e-119;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;

QY 54 KDRFNDEIDKLTGYKTSLLCMPTRSSDGLIIGVQAQAIN-KIPGAPFTDEDEKVMQY 112
Db 247 EDPRNAEVDQITGYKTSILCMPIKNHREEVGVQAQAINKSGNGGTFTEKDKFAAY 306

QY 113 LPFCGIAISNAQLFAASRKEYERSRALLEVNDLPFEQTDLEKIVKIMHRAQTLKCEK 172
Db 307 LAFCGIVLHNAQLYETSLLENKRNQVLLDASLIFEEOQSLEVLKKAATIIISPMQVK 366

QY 173 CSVLLEDIESPVVFKTSFELMSPKCSADAENSPK-----ESMEKSSYSDDL----- 220
Db 367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403

QY 221 ---INNSTAELVASTGLPVNISDAVDPRFAEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 404 ANKINMYAQVKNMTPELNPIDVSKDRFPMTTENTGNVQOCIRSLCTPIKNGKNK 463

QY 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKSWAKOSVAL 328
Db 464 VIGVCQLYKNMEENTGKVKPNRNDEQLEAFVIFCGLGIQNTQMYEAVRAMAKQWTL 523

QY 329 DVLVSHATCSK---AEDVKFAANITPLVSELAIDDIHEDFSLDQVDMITAAALRMFELG 385
Db 524 EVLSVHASAAEETRELQSLAAAVVPSAQTLLKITDFSPDLSLELTALCTIRMTDLN 583

QY 386 MVQEKIDYETLCRWLLTVKRNRM-VLYHNHRHAFNVQCLMFAMLTITAGQDILTEVEI 444
Db 584 LVQNFQMKHEVLCKWILSVKKNRYNVAIHNHRHAFNTAQCMFALAKGAKIGKLTDL 643

; Sequence 23, Application US/08480547A
; Patent No. 5652131
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlec, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08480,547A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565213land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32791
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-480-547A-10

Query Match 38.6%; Score 1355.5; DB 1; Length 875;
Best Local Similarity 42.9%; Pred. No. 6e-119;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;

QY 54 KDRFNDEIDKLTGYKTSLLCMPTRSSDGLIIGVQAQAIN-KIPGAPFTDEDEKVMQY 112
Db 247 EDPRNAEVDQITGYKTSILCMPIKNHREEVGVQAQAINKSGNGGTFTEKDKFAAY 306

QY 113 LPFCGIAISNAQLFAASRKEYERSRALLEVNDLPFEQTDLEKIVKIMHRAQTLKCEK 172
Db 307 LAFCGIVLHNAQLYETSLLENKRNQVLLDASLIFEEOQSLEVLKKAATIIISPMQVK 366

QY 173 CSVLLEDIESPVVFKTSFELMSPKCSADAENSPK-----ESMEKSSYSDDL----- 220
Db 367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403

QY 221 ---INNSTAELVASTGLPVNISDAVDPRFAEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 404 ANKINMYAQVKNMTPELNPIDVSKDRFPMTTENTGNVQOCIRSLCTPIKNGKNK 463

QY 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKSWAKOSVAL 328
Db 464 VIGVCQLYKNMEENTGKVKPNRNDEQLEAFVIFCGLGIQNTQMYEAVRAMAKQWTL 523

QY 329 DVLVSHATCSK---AEDVKFAANITPLVSELAIDDIHEDFSLDQVDMITAAALRMFELG 385
Db 524 EVLSVHASAAEETRELQSLAAAVVPSAQTLLKITDFSPDLSLELTALCTIRMTDLN 583

QY 386 MVQEKIDYETLCRWLLTVKRNRM-VLYHNHRHAFNVQCLMFAMLTITAGQDILTEVEI 444
Db 584 LVQNFQMKHEVLCKWILSVKKNRYNVAIHNHRHAFNTAQCMFALAKGAKIGKLTDL 643
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Db 237 EDPREAEVDQITGYKTKSILCMPIKHNREVEVGVQAQAINKKSGNGGTTTEKDEKDFAA 296
QY 113 LPFCGIAISNAQLFAASRKEYERSRALLEVNDLFEETQDLEKIVKIMHRAQTLLKGER 172
Db 297 LAFCGIVLHNAQLYTSLENNKRNQVLLDLASLIFEEOQSLEVLKKAATIIISFMQVOK 356
QY 173 CSVLLEDIESPVVKFTKSFELMSPKCSADANSEFK-----ESMEKSSYSDDL----- 220
Db 357 CTITFVDE-----DCSDSFSSVFHMECELEKS--SDTLTRERD 393
QY 221 ---INNSIAELVASTGLPVNISDAVQDPRFADAEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 394 ANRINYMAQYVKNMTPELNPVDSKDRFPWTNENMGNIQOCCIRSLCTPIKNGKKN 453
QY 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVFCGLGINNTIYDOVKKSWAKQSVAL 328
Db 454 VIGVCQLVNMKEETGKVKAFNRNDEQFLFAVFCGLGIQNTQMYEAVRAMAKQMTL 513
QY 329 DVLSYHATCSK---AEVDKFAANIPLVSELAIDDIHFDLSDVDAMITAAALRMFBLG 385
Db 514 EVLSYHASAAEETRELQSLAAAVVPSAQTILKITDIFSDFSLDLETALCTIRMTDLN 573
QY 386 MVQKFKIDYETLCRWLLTVRKNYRM-VLYHNHRHAFNVCOLMFAMLTITAGFQDILTEVEI 444
Db 574 LVQNFQMKHVELCVKWLISVKNYRNKRNVAHNHAFNTAQCMFAALKAGKIQKRLTDLEI 633
QY 445 LAVIVGCLCHDLDRGTNNAFQAKSGSALAQLYGTSALEHHHFNHVAVMILQSEGHNTFA 504
Db 634 LALLIAALSHLDHRGVNNSYQIORSHPLAQY-CHSIMEHHHFDQCLMILNSPGNQILS 692
QY 505 NLSKEYSDMLQKSLATDLTYLFFERTFEFELVSKGEYDNKINHRDIFRSMMLTA 564
Db 693 GLSIEYKTKLIIKQAILATDLALYIKRRGEFFELIMKNQFNLEDPHQKELFLAMLMTA 752
QY 565 CDLGAVTKPWEISROVAELVSEFEQDGRERLEKLTPTSAIFDRNRKDELPRLOLEWID 624
Db 753 CDLSAITKPMPIQOIRIAELVATEFFDQGRERLEKLTPTSAIFDRNRKDELPRLOLEWID 624
QY 625 SICMPLYQALVKVNVKLPMLDSVATNRSKWEEL--HQRLLASTASSSS 672
Db 813 AICQLQYALTHVSEDCPFLDDGCRKNQKQWALAEQOEKTLINGESSQT 862

RESULT 13

US-08-250-847B-10

Sequence 10, Application 05/08250847B

Patent No. 5702936

GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.

APPLICANT: Corbin, Jackie D.

APPLICANT: Ferguson, Kenneth M.

APPLICANT: Francis, Sharon H.

APPLICANT: Kadlec, Ann

APPLICANT: Loughney, Kate

APPLICANT: McAllister-Lucas, Linda M.

APPLICANT: Sonnenburg, William K.

APPLICANT: Thomas, Melissa K.

TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific

TITLE OF INVENTION: Phosphodiesterase Materials and Methods

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

-

APPLICATION NUMBER: US/08/250,847B

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/068,051

FILING DATE: 27-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5702936and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32083

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 875 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-250-847B-10

Query Match 38.6% Score 1355.5; DB 1; Length 875;

Best Local Similarity 42.9% Pred. No. 6e-119;

Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;

QY 54 KDRFNDEIDKTCYKTKSLCMLPIRSDSGEITIGVAQAIN-KIPEGAPFTEDEKVMOMY 112

Db 237 EDPREAEVDQITGYKTKSILCMPIKHNREVEVGVQAQAINKKSGNGGTTTEKDEKDFAA 296

QY 113 LPFCGIAISNAQLFAASRKEYERSRALLEVNDLFEETQDLEKIVKIMHRAQTLLKGER 172

Db 297 LAFCGIVLHNAQLYTSLENNKRNQVLLDLASLIFEEOQSLEVLKKAATIIISFMQVOK 356

QY 173 CSVLLEDIESPVVKFTKSFELMSPKCSADANSEFK-----ESMEKSSYSDDL----- 220

Db 357 CTITFVDE-----DCSDSFSSVFHMECELEKS--SDTLTRERD 393

QY 221 ---INNSIAELVASTGLPVNISDAVQDPRFADAEADQISGFH---IRSVLCVPIWN-SNHQ 273

Db 394 ANRINYMAQYVKNMTPELNPVDSKDRFPWTNENMGNIQOCCIRSLCTPIKNGKKN 453

QY 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVFCGLGINNTIYDOVKKSWAKQSVAL 328

Db 454 VIGVCQLVNMKEETGKVKAFNRNDEQFLFAVFCGLGIQNTQMYEAVRAMAKQMTL 513

QY 329 DVLSYHATCSK---AEVDKFAANIPLVSELAIDDIHFDLSDVDAMITAAALRMFBLG 385

Db 514 EVLSYHASAAEETRELQSLAAAVVPSAQTILKITDIFSDFSLDLETALCTIRMTDLN 573

QY 386 MVQKFKIDYETLCRWLLTVRKNYRM-VLYHNHRHAFNVCOLMFAMLTITAGFQDILTEVEI 444

Db 574 LVQNFQMKHVELCVKWLISVKNYRNKRNVAHNHAFNTAQCMFAALKAGKIQKRLTDLEI 633

QY 445 LAVIVGCLCHDLDRGTNNAFQAKSGSALAQLYGTSALEHHHFNHVAVMILQSEGHNTFA 504

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QY 505 NLSKEYSDMLQKSLATDLTYLFFERTFEFELVSKGEYDNKINHRDIFRSMMLTA 564

Db 693 GLSIEYKTKLIIKQAILATDLALYIKRRGEFFELIMKNQFNLEDPHQKELFLAMLMTA 752

QY 565 CDLGAVTKPWEISROVAELVSEFEQDGRERLEKLTPTSAIFDRNRKDELPRLOLEWID 624

Db 753 CDLSAITKPMPIQOIRIAELVATEFFDQGRERLEKLTPTSAIFDRNRKDELPRLOLEWID 624

QY 625 SICMPLYQALVKVNVKLPMLDSVATNRSKWEEL--HQRLLASTASSSS 672

Db 813 AICQLQYALTHVSEDCPFLDDGCRKNQKQWALAEQOEKTLINGESSQT 862

RESULT 14

US-08-463-949A-10

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Sequence 10, Application US/08463949A
Patent No. 5955583
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Corbin, Jackie D.
APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecsek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5955583and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-949A-10
Query Match 38.6%; Score 1355.5; DB 2; Length 875;
Best Local Similarity 42.9%; Pred. No. 6e-119;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;
QY 54 KDRFNDEIDKLTGYTKSLCMLPSSDGEITGVAAQAIN-KIPEGAPFTEDDEKVNQMY 112
Db 237 EDPRFAEVQITGYTKSLCMLPSSDGEITGVAAQAIN-KIPEGAPFTEDDEKVNQMY 296
QY 113 LPFCGTAISNAOLFPAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLKCR 172
Db 297 LAFCGVILHQAQYETSLLENKKNQVLLDASIFEEQSLVILKKAATIIISFMQVQK 356
QY 173 CSVLLLEDIESPVVKTFSPELSPKCSADAENSKF-----ESMEKSSYSDWL----- 220
Db 357 CTIFIVDE-----DCSFSFVSFVHMECEELEKS---STLTLRERD 393
QY 221 ---INNSIAELVASTGLPVNISDAYODPREDADQISGFH---IRSLVCVPIWN-SNHQ 273
Db 394 ANRINYMAQYVKNTEPLNIPDVSKDRFPWTNENNGINQQCIRSLCTPIKNGKNK 453
QY 274 IIGVAQVILNLDG-----KFDADQRLFEAFVIFCGLGINNTIMVDVKKSKAKOSVAL 328
Db 454 VIGVCQLVNKMEETGKVKAFNRNDEQLEAFVIFCGLGIONTMQVFAVERAMAKQVTL 513
329 DVLSYHATCSK---AEVDKFAANIPLVSELAIDDIHFDDFSLDSDVAMITAAIRMFMELG 385
514 EVLSYHASAAEEETRELOSIAAAVPSAQTLLKTDSEFSDFELSDLETALCTIRMTDLN 573
386 MVOKFKIDYETLCRWLLTVRKNYRM-VLYHNHRAFNVCQIMFAMLTUAGFQDILTEVEI 444
574 LVQNFQMKHEVLCKWILSVKKNYKKNVAYHNHRAFNVCQIMFAMLTUAGFQDILTEVEI 633
445 LAVIVGCLCHDLDRGTNNFAQKSGSALAQLYGTSTATLEHHHFNHVAVMILOSEGHNIFA 504
634 LALLIAALSHDLDRGVNNSYIQRSEHPLAQLY-CHSIMHHHFDQCLMILNPGNGLS 692
505 NLSKEYSDLMQLLKOSILATDTLYPFRTERTEFFELVSKGEYDNWIKNHRDIFRSMILMTA 564
693 GLSIEEYKTKLIIKQAILATDLALYIKRGEFFELIMKNQFNLEDPHQKELFLAMLMTA 752
565 CDLGAVTKPWEISROVAELVTSEFFEOGRERERLEKLTTPSAIFDRNRKDELPRLOLEWID 624
753 CDLSAITKPWPIQORIAELVATEFFDQGRERERLEKLTTPSAIFDRNRKDELPRLOLEWID 812
625 SICMPYQALVKVYNKLPMLDSVATNRKWEEL--HOKRLLASTASSSS 672
813 AICLQLYEALTHVSEDCFPULDGCRNKRQKWALEQQEKTILINGESSQT 862
RESULT 15
US-08-464-410A-10
Sequence 10, Application US/08464410A
Patent No. 6037119
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Corbin, Jackie D.
APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecsek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,410A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6037119and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32705
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:38:09 ; Search time 58.4282 seconds
(without alignments)
1559.921 Million cell updates/sec

Title: US-09-663-542-1
Perfect score: 3516
Sequence: 1 MLKQRRPLFRNLSATQWK.....ASTASSSPASVMWAKEDRN 684

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3516	100.0	684	22 AAG62678	Human type 11 phos
2	3516	100.0	684	22 AAB35472	Human cyclic nucle
3	3294.5	93.7	685	22 AAG62679	Rat type 11 phosph
4	3250	92.4	934	22 AAG62677	Human type 11 phos
5	3117.5	88.7	935	22 AAG62680	Rat type 11 phosph
6	2970	84.5	576	22 AAG67533	Amino acid sequenc
7	2541	72.3	490	21 AAV95521	Human cyclic nucle
8	2458	69.9	474	22 AAG67531	Amino acid sequenc
9	1762	50.1	367	21 AAY95522	Human cyclic nucle
10	1511.5	43.0	1284	22 ABB71869	Drosophila melanog

11	1511.5	43.0	1284	23 ABB08376	D. melanogaster CG
12	1380.5	39.3	1232	22 ABB63685	Drosophila melanog
13	1374	39.1	1126	21 AAY84879	Amino acid sequenc
14	1366.5	38.9	832	21 AAY78940	Human phosphodiesterase
15	1366.5	38.9	833	21 AAY90912	Human cGMP phospho
16	1366.5	38.9	833	22 AAB97024	Human phosphodiesterase
17	1366.5	38.9	875	16 AAR66565	Cyclic guanosine m
18	1366.5	38.9	875	20 AAY14991	Human cGMP-binding
19	1359.5	38.7	832	21 AAY78939	Human phosphodiesterase
20	1355.5	38.6	875	19 AA42011	Bovine cGMP-binding
21	1355.5	38.6	875	20 AAY14990	Bovine cGMP-binding
22	1349.5	38.4	875	16 AAR66564	Cyclic guanosine m
23	956	27.2	789	21 AAY53935	A human phosphodiesterase
24	956	27.2	791	21 AAY53936	A human phosphodiesterase
25	951	27.0	766	20 AAY13934	Human phosphodiesterase
26	951	27.0	766	22 AAB28256	Human phosphodiesterase
27	951	27.0	803	20 AAY13935	Human phosphodiesterase
28	951	27.0	803	22 AAB28257	Human phosphodiesterase
29	950	27.0	779	20 AAY13936	Human phosphodiesterase
30	950	27.0	779	21 AAB26853	Human phosphodiesterase
31	950	27.0	779	22 AAB73486	Human cyclic nucle
32	950	27.0	779	22 AAB28258	Human phosphodiesterase
33	950	27.0	789	21 AAB26854	Human phosphodiesterase
34	949	27.0	806	22 AAM51617	Human PDE10A polyp
35	934.5	26.6	941	16 AAR69729	Cyclic-GMP stimula
36	934.5	26.6	941	18 AAM18050	Human cGS-PDE amin
37	934.5	26.6	941	18 AAM11253	pHcgs6n cyclic GMP
38	934.5	26.6	941	19 AAW77042	Cyclic-GMP-stimula
39	934.5	26.6	941	19 AAW71226	Human cGS-PDE cDNA
40	934.5	26.6	941	19 AAM60754	Human cyclic-GMP-n
41	934.5	26.6	941	21 AAY80986	Human cGS-PDE, SEQ
42	934.5	26.6	941	22 AAE07918	Human phosphodiesterase
43	934.5	26.6	941	22 AAE07954	Human phosphodiesterase
44	934.5	26.6	941	22 AAG66539	Human interferon-a
45	934.5	26.6	941	22 AAB85106	Human cGMP-stimula

ALIGNMENTS

RESULT 1
AAG62678
ID AAG62678 standard; Protein: 684 AA.
XX AAG62678;
XX AC
XX 19-SEP-2001 (first entry)
XX Human type 11 phosphodiesterase SEQ ID NO: 4.
DE Human; type 11 phosphodiesterase; PDE11; signal transduction;
KW Human; type 11 phosphodiesterase; PDE11; signal transduction;
KW selective inhibition.
XX Homo sapiens.
OS Homo sapiens.
XX WO200146436-A1.
XX 28-JUN-2001.
XX 22-DEC-2000; 2000WO-JP09118.
XX 22-DEC-1999; 99JP-0364866.
PR 01-JUN-2000; 2000JP-0163875.
XX (TANA) TANABE SEIYAKU CO.
XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX WPI: 2001-418074/44.
XX N-PSDB; AA46709.
XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular

PT signal transduction mechanism and in screening highly-selective
XX inhibitors as drugs with superior efficacy
PS
XX
XX
XX

Claim 2; Page 49-51; 77pp; Japanese.

CC The present invention provides the protein and coding sequences of novel
CC human and rat type II phosphodiesterases (PDEII). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.

XX Sequence 684 AA;

Query Match 100.0%; Score 3516; DB 22; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.3e-304;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKQARRPLFRNVLSTATQWKKVITRLVQISGASLAELAEKQKHQDFLIQROTQTKDRRND 60
Db 1 MLKQARRPLFRNVLSTATQWKKVITRLVQISGASLAELAEKQKHQDFLIQROTQTKDRRND 60
QY 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
Db 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
QY 121 SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKERCSCVLLLED 180
Db 121 SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKERCSCVLLLED 180
QY 181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNINNSIAELVASTGLPVTSD 240
Db 181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNINNSIAELVASTGLPVTSD 240
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Db 241 AYQDPRFDEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGKPFDDADQRLFEAF 300
QY 301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360
Db 301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360
QY 361 IHFDDFSLEDVADAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAF 420
Db 361 IHFDDFSLEDVADAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAF 420
QY 421 NYCQLMFAMLTAGQDILTEVEILAVIVGCLCHDLHRGTNNAFQAKSGSALAOLYGT 480
Db 421 NYCQLMFAMLTAGQDILTEVEILAVIVGCLCHDLHRGTNNAFQAKSGSALAOLYGT 480
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QY 541 VSKGEYDWNKIHRIIFRSMILMTACDLGAVTKPWEISQVAVELTSEFFEOGDRERLEK 600
Db 541 VSKGEYDWNKIHRIIFRSMILMTACDLGAVTKPWEISQVAVELTSEFFEOGDRERLEK 600
QY 601 LTPSAIFORNRRKDELPRLOLEWIDSICMPLYOALYKVNKPKMLDSVATNRKSWHEELHQ 660
Db 601 LTPSAIFORNRRKDELPRLOLEWIDSICMPLYOALYKVNKPKMLDSVATNRKSWHEELHQ 660
QY 661 KRLLASTASSSSPASVMVAKEDRN 684
Db 661 KRLLASTASSSSPASVMVAKEDRN 684

RESULT 2
AAB35472
ID AAB35472 standard; protein; 684 AA.
XX
AC AAB35472;

XX 06-JUN-2001 (first entry)
XX Human cyclic nucleotide phosphodiesterase PDEXV.
DE
XX
XX Human cyclic nucleotide phosphodiesterase; PDEXV; sexual dysfunction;
KW cardiovascular disease; gastrointestinal disorder; corpus cavernosum;
KW kidney; liver; skeletal muscle; testis prostate; spleen.
XX
XX Homo sapiens.
OS
XX
XX EP1085089-A2.
PN
XX
XX 21-MAR-2001.
PD
XX
XX 14-SEP-2000; 2000EP-0307981.
PF
XX
XX 17-SEP-1999; 99GB-0022124.
PR
XX
XX (PFIZ) PFIZER LTD.
PA
XX (PFIZ) PFIZER INC.
PA
XX
PI Fidock MD, Robas NM;
DR
XX WPI: 2001-246900/26.
DR N-PSDB; AAF62311.
XX
XX Human cyclic nucleotide phosphodiesterase and its nucleotide sequence
PT useful for treating cardiovascular disorders, sexual dysfunction and
PT screening for drugs to treat associated disorders
PT
XX
XX Claim 1; Page 37-41; 44pp; English.
PS
XX
XX The present invention describes the protein and coding sequences of the
CC human cyclic nucleotide phosphodiesterase PDEXV. This enzyme is capable
CC of catalysing the degradation of cyclic nucleotides. The sequences are
CC useful in the treatment of cardiovascular, gastrointestinal, spleen,
CC corpus cavernosum, kidney, liver, skeletal muscle, testis and prostate
CC related disorders, and in the enhancement of the male erectile response
CC and the treatment of female sexual dysfunction. The present sequence is
CC the PDEXV protein.
XX
SQ Sequence 684 AA;
Query Match 100.0%; Score 3516; DB 22; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.3e-304;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKQARRPLFRNVLSTATQWKKVITRLVQISGASLAELAEKQKHQDFLIQROTQTKDRRND 60
Db 1 MLKQARRPLFRNVLSTATQWKKVITRLVQISGASLAELAEKQKHQDFLIQROTQTKDRRND 60
QY 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
Db 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
QY 121 SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKERCSCVLLLED 180
Db 121 SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKERCSCVLLLED 180
QY 181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNINNSIAELVASTGLPVTSD 240
Db 181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNINNSIAELVASTGLPVTSD 240
QY 241 AYQDPRFDEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGKPFDDADQRLFEAF 300
Db 241 AYQDPRFDEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGKPFDDADQRLFEAF 300
QY 301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360
Db 301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360
QY 361 IHFDDFSLEDVADAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAF 420

Db 361 IHFDDFSLDVMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNRHAF 420
QY 421 NVCOLMFAMLTITAGFODILTEVEILAVIVGCLCHDHRGTNNAFQAKSGSALAQLYGTG 480
Db 421 NVCOLMFAMLTITAGFODILTEVEILAVIVGCLCHDHRGTNNAFQAKSGSALAQLYGTG 480
QY 481 ATLEHHHFNHVMILQSEGHNIIFANLSSKEYSDLMQLLKOSILATDLTYLFFERTFEFFEL 540
Db 481 ATLEHHHFNHVMILQSEGHNIIFANLSSKEYSDLMQLLKOSILATDLTYLFFERTFEFFEL 540
QY 541 VSKGEYDWNINKNHRDIFRSMILMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK 600
Db 541 VSKGEYDWNINKNHRDIFRSMILMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK 600
QY 601 LTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVVKLKPMLDSVATNRKSWHEELHQ 660
Db 601 LTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVVKLKPMLDSVATNRKSWHEELHQ 660
QY 661 KRLLASTASSSSPASVWVAKEDRN 684
Db 661 KRLLASTASSSSPASVWVAKEDRN 684

RESULT 3

AAG62679
ID AAG62679 standard; Protein: 685 AA.

XX AC AAG62679;

DT 19-SEP-2001 (first entry)

DE Rat type 11 phosphodiesterase SEQ ID NO: 6.

KW Rat; type 11 phosphodiesterase; PDE11; signal transduction;
selective inhibition.

XX Rattus sp.

XX WO200146436-A1.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-JP09118.

XX 22-DEC-1999; 99JP-0364866.

XX 01-JUN-2000; 2000JP-0163875.

XX (TANA) TANABE SEIYAKU CO.

XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;

XX WPI: 2001-418074/44.

XX N-PSDB; AAH46710.

XX Type 11 phosphodiesterases and encoded genes with activity of
hydrolyzing cyclic nucleotides, useful for studying intracellular
signal transduction mechanism and in screening highly-selective
inhibitors as drugs with superior efficacy

XX Claim 2; Page 55-57; 77pp; Japanese.

XX The present invention provides the protein and coding sequences of novel
human and rat type 11 phosphodiesterases (PDE11). These are useful for
studying intracellular signal transduction mechanisms, in screening
highly-selective inhibitors as drugs for treating diseases associated
with the enzymes and for the identification or selection of selective
inhibitory action against multiple type phosphodiesterases. The present
sequence is a protein of the invention.

XX Sequence 685 AA;

Query Match 93.7%; Score 3294.5; DB 22; Length 685;

Best Local Similarity 93.7%; Pred. No. 7.8e-285;
Matches 644; Conservative 13; Mismatches 23; Indels 7; Gaps 2;
QY 1 MLKQARPLFRNVLSATQWKKVKITLVLQVLSGASLAEOKEKHODFLQROTFTKDRRFND 60
Db 1 MLKQARFSPNRVRSATQWRKVGSTROGQISGAFLAERLDKHODFLTRMOTRTKDRRFND 60
QY 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQMLPFCGIAI 120
Db 61 EIDKLTGYKTKSLLCMPIRNSDGEIIGVAAQAINKVPEGAPTEDEKVMQMLPFCGIAI 120
QY 121 SNAQLFAASKEYERSRALLEVVNDLPFEQTDLEKIVKKIMHRAQTLLKCERCSSLLED 180
Db 121 SNAQLFAASKEYERSRALLEVVNDLPFEQTDLEKIVKKIMHRAQTLLKCERCSSLLED 180
QY 181 IESPVVKFTKSFELMSPKCSADAENSPKESWESSYSDWLNINSIAELVASTGLPVNISD 240
Db 181 IESPVVKFTKSFELMSPKCSADAENSPKESWESSYSDWLNINSIAELVASTGLPVNISD 240
QY 241 AYQDPRDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGPDDADQRLFEAF 300
Db 241 AYQDPRDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGPDDADQRLFEAF 300
QY 301 VIFCGLGINTIMYDQVKKSWAKQSVADLVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360
Db 301 VIFCGLGINTIMYDQVKKSWAKQSVADLVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360
QY 361 IHFDDFSLDVMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNRHAF 420
Db 361 IHFDDFSLDVMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNRHAF 420
QY 421 NVCOLMFAMLTITAGFODILTEVEILAVIVGCLCHDHRGTNNAFQAKSGSALAQLYGTG 480
Db 421 NVCOLMFAMLTITAGFODILTEVEILAVIVGCLCHDHRGTNNAFQAKSGSALAQLYGTG 480
QY 481 ATLEHHHFNHVMILQSEGHNIIFANLSSKEYSDLMQLLKOSILATDLTYLFFERTFEFFEL 540
Db 481 ATLEHHHFNHVMILQSEGHNIIFANLSSKEYSDLMQLLKOSILATDLTYLFFERTFEFFEL 540
QY 541 VSKGEYDWNINKNHRDIFRSMILMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK 600
Db 541 VSKGAYDWSITSHRDVFRSMILMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK 600
QY 601 LTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVVKLKPMLDSVATNRKSWHEELHQ 660
Db 601 LTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVVKLKPMLDSVATNRKSWHEELHQ 660
QY 661 KRLLASTA---SSSSPASVWVAKEDR 683
Db 661 KRLLASTA---SSSSPASVWVAKEDR 684

RESULT 4

AAG62677
ID AAG62677 standard; Protein: 934 AA.

XX AC AAG62677;

DT 19-SEP-2001 (first entry)

XX Human type 11 phosphodiesterase SEQ ID NO: 2.

XX Human; type 11 phosphodiesterase; PDE11; signal transduction;
selective inhibition.

XX Homo sapiens.

XX WO200146436-A1.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-JP09118.

XX PF

PR 22-DEC-1999; 99JP-0364866.
XX 01-JUN-2000; 2000JP-0163875.
XX (TANA) TANABE SEIYAKU CO.
XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX WPI; 2001-418074/44.
XX N-PSDB; AAH46708.
XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy
XX Claim 2; Page 42-45; 77pp; Japanese.
XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.
XX Sequence 934 AA;
SQ
Query Match 92.4%; Score 3250; DB 22; Length 934;
Best Local Similarity 99.8%; Pred. No. 1.2e-280;
Matches 630; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 54 KDRFNDEIDKLTGYKTKSLCLMCPIRSSDGEIIGVAAQAINKIPEGAPFTEDDEKVMQMYL 113
DB 304 QDRFNDEIDKLTGYKTKSLCLMCPIRSSDGEIIGVAAQAINKIPEGAPFTEDDEKVMQMYL 363
QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEBQTDLEKIVKKIMHRAQTLLKCERC 173
DB 364 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEBQTDLEKIVKKIMHRAQTLLKCERC 423
QY 174 SVLLEDIESPVVKFTKSFELMSPKCSADAENFSKESMEKSSYSDWLIINNSIAELVASTG 233
DB 424 SVLLEDIESPVVKFTKSFELMSPKCSADAENFSKESMEKSSYSDWLIINNSIAELVASTG 483
QY 234 LPVNISDAYODPRFADAEADQISGFHRSVLCVPINWNSHQIIGVAAQLNRLDGKPFDDAD 293
DB 484 LPVNISDAYODPRFADAEADQISGFHRSVLCVPINWNSHQIIGVAAQLNRLDGKPFDDAD 543
QY 294 QRLFEAFVIFCGLGINNTIMYDOVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLV 353
DB 544 QRLFEAFVIFCGLGINNTIMYDOVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLV 603
QY 354 SELAIDDIHFDLDFSLDVAAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY 413
DB 604 SELAIDDIHFDLDFSLDVAAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY 663
QY 414 HNRHAFNVCQLMFAMLTITAGFODILTEVEILLAVIVGCLCHDLDRGTNNAFQKSGSAL 473
DB 664 HNRHAFNVCQLMFAMLTITAGFODILTEVEILLAVIVGCLCHDLDRGTNNAFQKSGSAL 723
QY 474 AQLYGTSAILEHHFHNHAWILOSSEGHNTIFANLSKEYSDLMQLLKOSILATDLTYLFFER 533
DB 724 AQLYGTSAILEHHFHNHAWILOSSEGHNTIFANLSKEYSDLMQLLKOSILATDLTYLFFER 783
QY 534 RTEFFELVSKGEYDWNKIHNRDIFRSMLTACDLGAVTKPWELSRVAELVTSERFEQGD 593
DB 784 RTEFFELVSKGEYDWNKIHNRDIFRSMLTACDLGAVTKPWELSRVAELVTSERFEQGD 843
QY 594 RERLEKLTPTSAIFDRNRKDELPRLOLEWIDSTCMPLYQALVKVNVKLPMLDSVATNRS 653
DB 844 RERLEKLTPTSAIFDRNRKDELPRLOLEWIDSTCMPLYQALVKVNVKLPMLDSVATNRS 903
QY 654 KWELHOKRLLASTASSSSPASVWVAKEDRN 684
|||||

DB 904 KWELHOKRLLASTASSSSPASVWVAKEDRN 934
RESULT 5
AAG62680
ID AAG62680 standard; Protein; 935 AA.
XX
XX AAG62680;
XX
XX 19-SEP-2001 (first entry)
XX Rat type 11 phosphodiesterase SEQ ID NO: 39.
XX Rat; type 11 phosphodiesterase; PDE11; signal transduction;
XX selective inhibition.
XX
XX Rattus sp.
XX
XX WO200146436-A1.
XX
XX 28-JUN-2001.
XX
XX 22-DEC-2000; 2000WO-JP09118.
XX
XX 22-DEC-1999; 99JP-0364866.
XX 01-JUN-2000; 2000JP-0163875.
XX
XX (TANA) TANABE SEIYAKU CO.
XX
XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX
XX WPI; 2001-418074/44.
XX N-PSDB; AAH46742.
XX
XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy
XX
XX Claim 2; Page 69-72; 77pp; Japanese.
XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.
XX Sequence 935 AA;
SQ
Query Match 88.7%; Score 3117.5; DB 22; Length 935;
Best Local Similarity 95.6%; Pred. No. 7.8e-269;
Matches 606; Conservative 9; Mismatches 12; Indels 7; Gaps 2;
QY 54 KDRFNDEIDKLTGYKTKSLCLMCPIRSSDGEIIGVAAQAINKIPEGAPFTEDDEKVMQMYL 113
DB 304 QDRFNDEIDKLTGYKTKSLCLMCPIRSSDGEIIGVAAQAINKIPEGAPFTEDDEKVMQMYL 363
QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEBQTDLEKIVKKIMHRAQTLLKCERC 173
DB 364 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEBQTDLEKIVKKIMHRAQTLLKCERC 423
QY 174 SVLLEDIESPVVKFTKSFELMSPKCSADAENFSKESMEKSSYSDWLIINNSIAELVASTG 233
DB 424 SVLLEDIESPVVKFTKSFELMSPKCSADAENFSKESMEKSSYSDWLIINNSIAELVASTG 483
QY 234 LPVNISDAYODPRFADAEADQISGFHRSVLCVPINWNSHQIIGVAAQLNRLDGKPFDDAD 293
DB 484 LPVNISDAYODPRFADAEADQISGFHRSVLCVPINWNSHQIIGVAAQLNRLDGKPFDDAD 543
QY 294 QRLFEAFVIFCGLGINNTIMYDOVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLV 353
|||||

Db 544 ORLFAFVIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAANIPLV 603
QY 354 SELAIDDDHEDDFSUDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY 413
Db 604 SELAIDDDHEDDFSUDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY 663
QY 414 HNRHAFNVQCMFAMLTAGFQDILTEVEILAVIGCLCHDLDRGTNNAFQAKSGSAL 473
Db 664 HNRHAFNVQCMFAMLTAGFQDILTEVEILAVIGCLCHDLDRGTNNAFQAKSGSAL 723
QY 474 AOLYGTSAATLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKQSLATDLTLTYFER 533
Db 724 AOLYGTSAATLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKQSLATDLTLTYFER 783
QY 534 RTEFFELVSKGEYDWNINRHRDIFRSMELMTACDLGAVTKPWEISRQVAELVTSEFQEGD 593
Db 784 RTEFFELVSKGAYDWSITSHRDVFRSMLMTACDLGAVTKPWEISRQVAELVTSEFQEGD 843
QY 594 RERLEKLTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALYKVNKLKPMPLDSVATNRS 653
Db 844 RERSELKTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALYKVNKLKPMPLDSVATNRS 903
QY 654 KWELHQKRLASTA----SSSSPASVMVAKEDR 683
Db 904 KWELHQKRLQVSAASPVSPSPA---VAGEDR 934

RESULT 6
AAG67533
ID AAG67533 standard; Protein; 576 AA.
XX AAG67533;
XX
XX
XX 26-NOV-2001 (first entry)
DE Amino acid sequence of a human phosphodiesterase polypeptide.
XX Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension;
KW nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism;
KW osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis;
KW Parkinson's disease; dementia; infectious disease; malignant tumour.
XX
OS Homo sapiens.
XX
XX WO200166716-A1.
XX
XX 13-SEP-2001.
XX
XX 06-MAR-2001; 2001WO-JP01720.
XX
XX 07-MAR-2000; 2000JP-0061464.
XX 10-JUL-2000; 2000JP-0208610.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Miyaaji H, Haruoka M, Ota T, Kawabata A, Sugano S, Nakamura Y;
PI WPI; 2001-570769/64.
XX N-PSDB; AAH78232.
XX
XX Polypeptides with phosphodiesterase activity and DNA for treatment of
PT diabetes, ischemic heart disease, hypertension, nephritis,
PT pancreatitis, ulcers, allergies, asthma
XX
XX Claim 1; Page 90-93; 105pp; Japanese.
XX
XX The present sequence encodes a human polypeptide which has
CC phosphodiesterase activity. The phosphodiesterase polypeptide and
CC polynucleotide are used for the treatment and prevention of diabetes,
CC ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers,
CC allergies, asthma, rheumatism, osteoporosis, pain, anxiety,
CC schizophrenia, manic depressive psychosis, Parkinson's disease,
CC dementia, infectious diseases, and malignant tumours.

XX Sequence 576 AA:
SQ
Query Match 84.5%; Score 2970; DB 22; Length 576;
Best Local Similarity 100.0%; Pred. No. 5, 4e-256;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 MQMYLPFCGIAISNAQLFAASRKEYERSRALLLEVNVNDFEEQTDLEKIVKKIMHRAQTLL 168
Db 1 MQMYLPFCGIAISNAQLFAASRKEYERSRALLLEVNVNDFEEQTDLEKIVKKIMHRAQTLL 60
QY 169 KCERCSVLLLEDDIESPVVKFTKSPFELMSPKCSADAENSKFMEKSSSYSDWLNNISIAL 228
Db 61 KCERCSVLLLEDDIESPVVKFTKSPFELMSPKCSADAENSKFMEKSSSYSDWLNNISIAL 120
QY 229 VASTGLPVNISDAYQDPRFDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGRP 288
Db 121 VASTGLPVNISDAYQDPRFDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGRP 180
QY 289 FDDAQRLFEAFVIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAA 348
Db 181 FDDAQRLFEAFVIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAA 240
QY 349 NIPLYSELAIDDDHEDDFSUDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNY 408
Db 241 NIPLYSELAIDDDHEDDFSUDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNY 300
QY 409 RMVLYHNRHAFNVQCMFAMLTAGFQDILTEVEILAVIGCLCHDLDRGTNNAFQAK 468
Db 301 RMVLYHNRHAFNVQCMFAMLTAGFQDILTEVEILAVIGCLCHDLDRGTNNAFQAK 360
QY 469 SGSALAQLYGTSAATLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKQSLATDLT 528
Db 361 SGSALAQLYGTSAATLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKQSLATDLT 420
QY 529 LYFERTEFFELVSKGEYDWNINRHRDIFRSMELMTACDLGAVTKPWEISRQVAELVTSEF 588
Db 421 LYFERTEFFELVSKGEYDWNINRHRDIFRSMELMTACDLGAVTKPWEISRQVAELVTSEF 480
QY 589 FEQGRERLEKLTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALYKVNKLKPMPLDSV 648
Db 481 FEQGRERLEKLTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALYKVNKLKPMPLDSV 540
QY 649 ATNRSKWEELHOKRLIASTASSSSPASVMVAKEDRN 684
Db 541 ATNRSKWEELHOKRLIASTASSSSPASVMVAKEDRN 576
RESULT 7
AAY95521
ID AAY95521 standard; Protein; 490 AA.
XX AAY95521;
XX
XX 10-OCT-2000 (first entry)
XX Human cyclic nucleotide phosphodiesterase HSPDE10A1.
XX
XX Cyclic nucleotide phosphodiesterase; HSPDE10A1; human; cancer;
KW immune disorder; diagnosis; therapy.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FH 196..458
FT /note= "catalytic domain"
FT 88..99
FT /note= "putative cGMP binding motif"
FT 260..269
FT /note= "phosphodiesterase signature motif"
XX
PN WO200040733-A1.
XX

Db 301 YSDMLQLLKQSILATDLTLYFERRTEFFELVSKGEYDWNKIHNRDIFRSMMLTACDLGAV 360
QY 571 TKPWEISQVRAELVTSEFFEOGDRERLEKLTTPSAIFDRNRKDELPRQLQLEWIDSICMPL 630
Db 361 TKPWEISQVRAELVTSEFFEOGDRERLEKLTTPSAIFDRNRKDELPRQLQLEWIDSICMPL 420
QY 631 YOALVKVNVKLPMLDSVATNRKSWHEELHQRLLASTASSSSPASVMVAKEDRN 684
Db 421 YOALVKVNVKLPMLDSVATNRKSWHEELHQRLLASTASSSSPASVMVAKEDRN 474

RESULT 9
ID AAY95522 standard; Protein; 367 AA.
XX
AC AAY95522;
XX
DT 10-OCT-2000 (first entry)
XX
DE Human cyclic nucleotide phosphodiesterase HSPDE10A2.
XX
KW Cyclic nucleotide phosphodiesterase; HSPDE10A2; human; cancer;
KW immune disorder; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 88..99
FT /note= "putative cGMP binding motif"
FT Peptide 260..269
FT /note= "phosphodiesterase signature motif"
XX
XX WO200040733-A1.
PN 13-JUL-2000.
XX
XX 07-JAN-2000; 2000WO-US00371.
PF
XX
XX 07-JAN-1999; 99US-0226741.
PR
XX
XX (INCY-) INCYTE PHARM INC.
PA
XX
XX Phillips SC, Lanfear J, Fawcett L, Bandman O, Harrow I;
PI
XX
XX WPI; 2000-452539/39.
DR
XX
XX N-PSDB; AAA49973.
PT
XX
XX New human cyclic nucleotide phosphodiesterases, referred as HSPDE10A1
PT and HSPDE10A2, useful for treating and preventing cancer and immune
PT disorders -
XX
XX Claim 1; Page 84; 96pp; English.
PS
XX
XX The present sequence is that of HSPDE10A2, a novel human cyclic
CC nucleotide phosphodiesterase. The amino acid sequence was deduced
CC from an isolated cDNA clone (see AAA49973). HSPDE10A2 is a
CC C-terminal splice variant of HSPDE10A1 (see AAY95521), being
CC identical between amino acid residues 1-338, but different in the
CC C-terminal portion from residue 339 to 367. It shares 40%
CC identity with HSPDE3A1. The invention provides expression vectors,
CC host cells, antibodies, agonists and antagonists, as well as
CC methods for diagnosing, treating or preventing disorders associated
CC with expression of HSPDE10A1, especially cancer and immune
CC disorders.
XX
XX Sequence 367 AA;
SQ

Query Match 50.1%; Score 1762; DB 21; Length 367;
Best Local Similarity 99.4%; Pred. No. 1.7e-148;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 195 MSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDEADQI 254
|||||

Db 1 MSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDEADQI 60
QY 255 SGFHRSVLCVPIMWSNHOIIGVAOVNLDCKPDDADQRLPEAFVIFCGLGINNNTIMY 314
Db 61 SGFHRSVLCVPIMWSNHOIIGVAOVNLDCKPDDADQRLPEAFVIFCGLGINNNTIMY 120
QY 315 DOVKKSWAKQSVALDVLSYHATCSKAEDVKFKAANITPLVSELAIDDIHFDDFSLOVDAMI 374
Db 121 DOVKKSWAKQSVALDVLSYHATCSKAEDVKFKAANITPLVSELAIDDIHFDDFSLOVDAMI 180
QY 375 TAALRMFMELGMVQKFIDYETLCRWLLTVRKNYRMVLYHNNRHAFNVCOLMFAMLTAG 434
Db 181 TAALRMFMELGMVQKFIDYETLCRWLLTVRKNYRMVLYHNNRHAFNVCOLMFAMLTAG 240
QY 435 FODILTEVEILAVIVGCLCHDLHRTGNNAFQAKSGSALAQLYGTSALEHHHFNHAVMI 494
Db 241 FODILTEVEILAVIVGCLCHDLHRTGNNAFQAKSGSALAQLYGTSALEHHHFNHAVMI 300
QY 495 LOSEGHNIFANLSKESYSDMLQKQSIATDLTLYFERR 534
Db 301 LOSEGHNIFANLSKESYSDMLQKQSIATDLTLYFERR 340

RESULT 10
ID ABB71869 standard; Protein; 1284 AA.
XX
AC ABB71869;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 42399.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX
XX 11-JUL-2000; 2000US-0614150.
PR
XX
XX (PEKE) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX WPI; 2001-656860/75.
DR
XX
XX N-PSDB; ABL15972.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure; SEQ ID NO 42399; 21pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
XX
XX The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1284 AA;
SQ

```
Query Match 43.0%; Score 1511.5; DB 22; Length 1284;
Best Local Similarity 44.4%; Pred. No. 2.5e-125;
Matches 303; Conservative 126; Mismatches 202; Indels 51; Gaps 6;

QY 20 KVKITRLVQISGSLAEKQKHQDFLQRTQ-----KTKRRFNDEI 62
DB 263 KKCLVSKLFDVCPSTVEEMEQDEVRVAGTGIAGHVAESGEPVNPIDAYQDERNCEI 322
QY 63 DKLGYTKSLCMLPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIATSN 122
DB 323 DSLGYRTKALLCPIKSSGDIVGVAQVINKM-NGECFSEIDEKVFSSYLQFCGIGURN 381
QY 123 AOLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKKIMHRAQTLLKERCSSLLEDIE 182
DB 382 AOLYKESQLEIKRNOVLDLARMIFEQSTIEHVMVFRILTHMQSLQCORVOILLVHEAD 441
QY 183 SPVVKFTKSFELMSPKCSADAESEKESMEKSSYSDWLNNISIAELVASTGLPVNISDAY 242
DB 442 KG--SFSRVDFEANDLSEEEATSRTPYE---SRPPINIGITGHVATTGETVNPVNAV 495
QY 243 QDPREDADQISGFHRSVLCVPINNSHNOIIGVAQVNLNLDGKPPDDAQRLFEAFVI 302
DB 496 EDDRFDASVDENSCFKHRSILCMAIKNSLGOIIGVIQILINKFNELDTKNDENVEAFAI 555
QY 303 FCGIGINNTIMYDOVKKSWAKOSVALDVLSYHATCSKAEDVKF-----KTKRRFNDEI 345
DB 556 FCGMGIHNTMYEKAIVAMAKOSVTLVLSYHASATMDAEHRLRKQKQOQOAVGLRQAPL 615
QY 346 -----KAANIPLVSELAIDDIHFDDFSLDVDAMITAAALRMFMELGMVKFKIDYET 396
DB 616 SLPPRKKLQRLRVPESAVHFLHDFKFDIHFEEDDTLTKACLRMFLDLDFVERHIDYEV 675
QY 397 LCRWLLTVRKNYRMVLYHNHRAFNVCOLMFAMLTITAGFQDILTEVETLAVIGCLCHDL 456
DB 676 LCRWLLSVKKNRNVYTHNHRHAFNVAQMFAILLTQWVKIFGEICLAILIGCLCHDL 735
QY 457 DHRGTNNAFAQSGSALAQLYCTSATLHEHHNFHNAVMIQSEGHNFANLSKKEYSDLMQ 516
DB 736 DHRGTNNSFOIKASSPLAQLYSTS-TMEHHFHDQCLMILNSPGNOILANLSSDDYCRVIR 794
QY 517 LKQSLATDLTLFERTERFELYSKGEYDWNITKNHRDIFRSLMNTACDLGAVTKPWEI 576
DB 795 VLEDAILSTDLAVFKKGPFLSVSQTYSYVAEEPRALLRAMSMTVCDLSAITKPWEI 854
QY 577 SRQVAELVTSFEEOGDRELERLELTPSAIFDRNRKDELPRLOLEWIDISICMPLYQALVK 636
DB 855 EKRVAADVLSSEFEEOGDMEKQELNITPIDINRKEDELPMMQVNFIDISICLIYEAPAT 914
QY 637 VNVKLKPLMDSVATNRSKWEEL 658
DB 915 LSDKLEPLVEGVRDRNGHWIDL 936

RESULT 11
ABB08376
ID ABB08376 standard; Protein; 1284 AA.
XX AC ABB08376;
XX DT 07-MAY-2002 (first entry)
XX DE D. melanogaster CG10231 gene product.
XX KW Transketotase-like; enzyme; fruitfly; cytostatic; antianaemic; cancer;
XX PN anaemia; end-stage renal disease; sensory neuropathy; uraemia.
XX OS Drosophila melanogaster.
XX WO200192310-A2.
XX PD 06-DEC-2001.
XX
```

```
PF 30-MAY-2001; 2001WO-EP06125.
PR 31-MAY-2000; 2000US-207950P.
XX (FARB ) BAYER AG.
XX Ramakrishnan S;
XX WPI; 2002-130523/17.
XX Novel isolated human transketotase-like enzyme polypeptide, useful for
XX treating cancer, anaemia, end-stage renal disease and sensory neuropathy
XX associated with uraemia
XX Disclosure; Fig 5; 91pp; English.
XX The invention relates to an isolated transketotase-like enzyme
XX polypeptide. The activity of the polypeptide of the invention may be
XX described as cytostatic and antianaemic. Polypeptides and polynucleotides
XX of the invention can be used to identify agents that modulate the
XX activity of a transketotase-like enzyme. They are also useful for
XX treating transketotase-like enzyme disorder such as cancer, anaemia,
XX end-stage renal disease and sensory neuropathy associated with uraemia.
XX Therapeutic agents of the invention are useful for modulating the
XX activity of transketotase-like enzyme in the above mentioned diseases.
XX Polypeptides and polynucleotides of the invention are useful for
XX identifying test compounds which act as agonists or antagonists, for
XX raising specific antibodies, and as a bait protein in a two-hybrid or
XX three-hybrid assay. They are also useful in diagnostic assays for
XX detecting diseases and abnormalities or susceptibility to disease and
XX abnormalities related to the presence of mutations in the
XX transketotase-like enzyme encoding sequence. Fusion proteins including
XX the polypeptide of the invention may be useful in the generation of
XX antibodies and in various assay systems. The current sequence represents
XX the D. melanogaster CG10231 gene product that was used to aid the
XX identification of human transketotase-like enzyme.
```

Sequence 1284 AA;

Query Match 43.0%; Score 1511.5; DB 23; Length 1284;

Best Local Similarity 44.4%; Pred. No. 2.5e-125;

Matches 303; Conservative 126; Mismatches 202; Indels 51; Gaps 6;

```
QY 20 KVKITRLVQISGSLAEKQKHQDFLQRTQ-----KTKRRFNDEI 62
DB 263 KKCLVSKLFDVCPSTVEEMEQDEVRVAGTGIAGHVAESGEPVNPIDAYQDERNCEI 322
QY 63 DKLGYTKSLCMLPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIATSN 122
DB 323 DSLGYRTKALLCPIKSSGDIVGVAQVINKM-NGECFSEIDEKVFSSYLQFCGIGURN 381
QY 123 AOLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKKIMHRAQTLLKERCSSLLEDIE 182
DB 382 AOLYKESQLEIKRNOVLDLARMIFEQSTIEHVMVFRILTHMQSLQCORVOILLVHEAD 441
QY 183 SPVVKFTKSFELMSPKCSADAESEKESMEKSSYSDWLNNISIAELVASTGLPVNISDAY 242
DB 442 KG--SFSRVDFEANDLSEEEATSRTPYE---SRPPINIGITGHVATTGETVNPVNAV 495
QY 243 QDPREDADQISGFHRSVLCVPINNSHNOIIGVAQVNLNLDGKPPDDAQRLFEAFVI 302
DB 496 EDDRFDASVDENSCFKHRSILCMAIKNSLGOIIGVIQILINKFNELDTKNDENVEAFAI 555
QY 303 FCGIGINNTIMYDOVKKSWAKOSVALDVLSYHATCSKAEDVKF-----KTKRRFNDEI 345
DB 556 FCGMGIHNTMYEKAIVAMAKOSVTLVLSYHASATMDAEHRLRKQKQOQOAVGLRQAPL 615
QY 346 -----KAANIPLVSELAIDDIHFDDFSLDVDAMITAAALRMFMELGMVKFKIDYET 396
DB 616 SLPPRKKLQRLRVPESAVHFLHDFKFDIHFEEDDTLTKACLRMFLDLDFVERHIDYEV 675
QY 397 LCRWLLTVRKNYRMVLYHNHRAFNVCOLMFAMLTITAGFQDILTEVETLAVIGCLCHDL 456
DB 676 LCRWLLSVKKNRNVYTHNHRHAFNVAQMFAILLTQWVKIFGEICLAILIGCLCHDL 735
```


Db 676 LCRWLLSVKKNVNTVYHNHRAFNVAOMFAILLTTOHWKIFGEIECLALIGCLCHDL 735
 QY 457 DHRGTNAPQAKSGSALAOLYGTSTALEHHNHNHAWMILOQSEGHNFANLSSKEYSDLMQ 516
 Db 736 DHRGTNNSQIKASSPLAOLYSTS-TMEHHHFDQCLMILNSFGNQILANLSSDDYCRVIR 794
 QY 517 LKQSLATDLGLYFERRTEFFELVSKGYDNNKHNHRDIFRSMLMTACDLGAVTKPWEI 576
 Db 795 VLEDAILSTDLAVYFKKRGPFLESVSQPTSYVVAEPRALLRAMSMTVCDSLTAITKPWEI 854
 QY 577 SRQVAELVTSEFEQDGERLEKLTPSAIFDRNRKDELPRQLQLEWIDSICMPLYQALVK 636
 Db 855 ERKRVADLVSEFEQDMEKQELNITPIDIMNREKEDELPMQVNFIDSICLPVEAFAT 914
 QY 637 VNVKLPMLDSVATNRSKWEEL 658
 Db 915 LSDKLEPLVEGVDRNKGHWIDL 936

RESULT 12

ABB63685
 ID ABB63685 standard; Protein; 1232 AA.

AC ABB63685;

XX 26-MAR-2002 (first entry)

DT Drosophila melanogaster polypeptide SEQ ID NO 17847.

DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL07788.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions

PS Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1232 AA;

Query Match 39.3%; Score 1380.5; DB 22; Length 1232;
 Best Local Similarity 38.9%; Pred. No. 1.le-113;
 Matches 299; Conservative 109; Mismatches 211; Indels 149; Gaps 10;

QY 28 VOISGASLAEOEKHODFLIORQTKTKDRRNFENDEIDKLTGYKTKSLCMLPIRSSDGEIIG 87
 Db 326 IGIAGWVAOTKO-----MINIKEAYKDARENCEIDKLTGYKTKNALICPICNVEGDIIG 379
 QY 88 VQAQAINKIPGAPPTDEDEKVMOMYLPPFCGIAISNAQLFAASKEYERSALLLEVNDLFL 147
 Db 380 VQAIIINNTKCMGFEFDEHDEVEIFRRLTFCGIGIQNAQLFEMSVOEQRRNQIILLNARSIF 439
 QY 148 EQGTDLEKLVKKIMHRAOTLLKCCERCSVLLJE-----DIESP-----VVKFTK 190
 Db 440 EQONNLECLVTKIMTEARELLKCCERCSVFLVDLDOCCESASHEKIIIEKPNOPATRAIKSAD 499
 QY 191 SEF-----LMSPKGSADAENSEFKESMEKSSYSDMLINNSIAELVASTGLPVNISD 240
 Db 500 SPEEKKMRNFTVLFFELGGEYQAANVSRRPSVSELSSSTLA--QIAQVATTQTGVNICD 556
 QY 241 A-----YQDPFDEADQISGPHIRSVLCVPIWNSNHQIIGVAQVNLRLDGPFDQDQ 294
 Db 557 VIEWVRDHQIRAEDEIDS-----TQAILCMPIMNAQKKVIGVAQLINKANGVPFTDSDA 611
 QY 295 RLFEAFVIFCGLGINTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAANIPLVS 354
 Db 612 SIFEAFVIFCGLGINTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAANIPLVS 354
 QY 355 ELAIDDIHFDFSLDVDAMITAAALRMFMELGMVQKEKIDYETLCRWLLTVKRNRYMLVXH 414
 Db 672 SYNLYSFTTDFELVDDDTCAVLRMFMOCNLVSQFIPYDVLCRVLSVRKNYRPVKYH 731
 QY 415 NWRHAFNVCOLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFAKSGSALA 474
 Db 732 NWRHALNVAQTMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFAKSGSALA 474
 QY 475 QLYGTSATLEHHHFNH-----490
 Db 792 ILY-TTSTMEHHHFDHFLAAFLDLRAAFRRALRDJARELLDLVEELVDPDTLIFLVIEY 850
 QY 491 -----AVMILQS-----497
 Db 851 FRLRLRTILFPELDEEDDDVVDSVVVSVLVSLVLDLSVLLSAAALTWATYKTIER 910
 QY 498 -----EGHNIFANLSKEYSDLMOLLKOSILATOLTYFERRTEFFELVSGEYDWNINKH 553
 Db 911 TKTRDNFMLDALSPEDYRSVMKTVESAILSTDLAMYFKKNAPFLVELVGEFDMQGECK 970
 QY 554 RDIERSMLTACDLGAVTKPWEISROVAELVTSEFEQDGERLEKLTPSAIFDRNRKD 613
 Db 971 KDLCCGMMMTACDVSAIAKPWEVQHKVAKIVADEFFDQDGLKQLQNTQVAMMDREKRD 1030
 QY 614 ELPRLOLEWIDSICMPLYQALVKVNVKLPMLDSVATNRSKWEELHOK 661
 Db 1031 ELPMQGVGFDVLCILPLYRVLCDTFFWITPLYECTLENRRNWQDLAEK 1078

RESULT 13

AAY84879

ID AAY84879 standard; Protein; 1126 AA.

AC AAY84879;

DT 21-AUG-2000 (first entry)

DE Amino acid sequence of a PDE5D-GFP fusion protein.

XX I-kappaB kinase; cyclic nucleotide phosphodiesterase; cyclic AMP;
 KW cyclic GMP; PDE3; PDE7; PDE8; PDE4 splice variant; PDE4D;
 KW inflammatory disease; chronic inflammation; airway disease; asthma;
 KW chronic bronchial hyper-reactivity; joint disorder; rheumatoid arthritis;
 KW pelvospodulitis; bowel disease; ulcerative colitis; Crohn's disease;
 KW autoimmune disease; diabetes mellitus type I; Hashimoto's thyroiditis;
 KW systemic lupus erythematosus; myasthenia gravis; Grave's disease;
 KW immune thrombocytopenic purpura; acute respiratory distress syndrome;
 KW septic shock; depression; PDE1; PDE2; PDE5; PDE9; PDE10; jet lag;

KW PDE5 splice variant; tension; erectile dysfunction; circadian rhythm;
 KW green fluorescent protein; GFP.
 XX Synthetic.
 OS Homo sapiens.
 OS Aequorea victoria.
 XX WO200023091-A2.
 PN 27-APR-2000.
 XX 15-OCT-1999; 99WO-DK00567.
 XX 15-OCT-1998; 98DK-0001321.
 PR 15-OCT-1998; 98DK-0001322.
 PR 15-OCT-1998; 98DK-0001323.
 XX (BIOT-) BIOIMAGE AS.
 PA Arkhammar POG, Terry BR, Scudder KM, Bjorn SP, Thastrup O;
 PI WPI: 2000-399281/34.
 DR N-PSDB; AAL4957.
 DR Modulating the activity of I-kappaB kinases or cyclic nucleotide
 XX phosphodiesterases for the treatment of inflammatory disorders,
 PT autoimmune disorders (e.g. diabetes and Crohn's disease) and depression
 PT
 XX Example 2; Page 103-105; 128pp; English.
 PS The specification describes a method for modulating the specific
 XX effectiveness of I-kappaB kinases or cyclic nucleotide phosphodiesterases
 CC which have the ability to cleave cyclic AMP and/or GMP. This involves
 CC modulating the specific effectiveness of the cyclic nucleotide
 CC phosphodiesterase or I-kappaB kinase by modulating the spatial
 CC distribution within cells of the animal. If the cyclic nucleotide
 CC phosphodiesterase used is a PDE3, PDE7, PDE8 or a splice variant of
 CC PDE4 (such as PDE4D), the method is used to treat inflammatory
 CC diseases such as chronic inflammation (especially airway diseases such
 CC as asthma and chronic bronchial hyper-reactivity of non-asthma etiology,
 CC joint disorders such as rheumatoid arthritis and pelvispondylitis and
 CC bowel diseases such as ulcerative colitis and Crohn's disease),
 CC autoimmune diseases associated with inflammation (such as diabetes
 CC mellitus type I, systemic lupus erythematosus, myasthenia gravis,
 CC Hashimoto's thyroiditis, Grave's disease and immune thrombocytopenic
 CC purpura), dysregulations of the immune system (such as acute respiratory
 CC distress syndrome (ARDS) and septic shock) and/or depression.
 CC Alternatively, if the cyclic nucleotide phosphodiesterase is PDE1, PDE2,
 CC PDE6, PDE9, PDE10 or a splice variant of PDE5, the method is used to
 CC treat hypo- or hypertension, erectile dysfunction, circadian rhythm
 CC resetting or jet-lag. The present sequence represents a fusion protein of
 CC PDE5p and green fluorescent protein (GFP), which is used in the course
 CC of the invention.
 XX
 XX Sequence 1126 AA;
 SQ
 Query Match 39.1%; Score 1374; DB 21; Length 1126;
 Best Local Similarity 42.5%; Pred. No 3.8e-113;
 Matches 284; Conservative 131; Mismatches 188; Indels 66; Gaps 13;
 QY 54 KORFENDEIKTGKTKSLCCMPINSSDGEIIGVAQAIN-KIPEGAPFTDEDERVMQMY 112
 DB 247 EDPRFAEVDQITGYKTQILCMPTKNHREEVGVQAQAINKKSGNGTFTKEDKFAAY 306
 QY 113 LPFCGTAISNAOLFASRKEYERSRALLVVDLFEQTDLEKIVKIMHRAQTLLKCR 172
 DB 307 LAFCGIVLHAQLYETSLLENQVLLDLASLFEQQOSLEVLILKIAATITISFMQVK 366
 QY 173 CSVLLEDIESPVKFTKSFELMSPKCSADAENSK-----ESMEKSSYSDWL----- 220
 DB 367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403

QY 221 ----INNSTAELVASTGLPVPNISDAYQDPREDAAQDISGFH---IRSLVLCVPIWN-SNHQ 273
 DB 404 ANKINMYAQYVKNTMEPLNIPDVSKDKRFPWTENTGVNNOQCIRSLCTPIKNGKNK 463
 QY 274 IIGVAQVNLRLDG-----KPFDDAORLEAFVIFCGLGINNTIMYDQVKKSAKOSVAL.328
 DB 464 VIGVCOLVNKMBEENTGKVKPFNRNDEQFLFAFVIFCGLGIONTQMYEAVRAMAKOMVTL 523
 QY 329 DVLSYHATCSK---AEVDKFKAAANIPLVSELAIDDDIFDDFSLDQVDMITAAALRMFMELG 385
 DB 524 EVLSYHASAAEBETRELOSLAAAVPSAOTLKITDFSPDFSLDLETALCTIRMTDLN 583
 QY 386 MVQKFKIDYETLCRWLLTVRKNYRM-VLYHNHRHAFNVCOLMFAMLTITAGFODILTEVEI 444
 DB 584 LVQNFQMKHEVLCRWILSVKKNVAVYHNHRHAFNTAQCMFAALKAGKIQNKLTDEI 643
 QY 445 LAVIVGCLCHDLDRCTNNAFQAKSGSALAOLYGTTSATLEHHFHNHAYMILQSEGNIFA 504
 DB 644 LALLTAALSHDLDRGVNNSYTORSEHPLAQLY-CHSIMEHHFDDQCLMLNSPGNOILS 702
 QY 505 NLSKEYSDLMOLLKOSILATDLTLTYFERRTEFFELVSKGEYDWNKHNHRIDFRSLMLTA 564
 DB 703 GLSIEYKTKLIIKOAILATDLALYIKRRGEFFELIRKQNFQNLDPHOKELFLAMLTA 762
 QY 565 CDLGAVTKPWEISRQVAELVTSEFFQGDRELEKLTPSAIFDRNRKDELPLQLLEWID 624
 DB 763 CDLSAITRPWPIQRIAEIVATEFFDQGDREKELNIEPTDLNREKKNKIPSMQVGFID 822
 QY 625 SICMPLYQALVKNVVKLPMLDSVATNRSKWEEL--HQKRLLASTASSSS----- 672
 DB 823 AICLOLYEALTHVSDCFPLLDGCRKNQKQWALAPQOEKMLINGESGOAKRNWVPRARD 882
 QY 673 -PASVNVAK 680
 DB 883 PPAVTVMSK 891
 RESULT 14
 ID AAY78940 standard; Protein; 832 AA.
 XX AAY78940
 AC AAY78940;
 DT 05-JUN-2000 (first entry)
 XX Human phosphodiesterase V amino acid sequence #2.
 XX Phosphodiesterase V; human; hypertension; pulmonary hypertension;
 KW atherosclerosis, cerebral infarction; allergic rhinitis; kidney failure;
 KW diabetic complication; glaucoma.
 XX Homo sapiens.
 XX WO200005383-A1.
 PD 03-FEB-2000.
 PF 19-JUL-1999; 99WO-JP03865.
 PR 21-JUL-1998; 98JP-0204964.
 PR 16-APR-1999; 99JP-0108974.
 XX (TAKE) TAKEDA CHEM IND LTD.
 PI Tarui N, Doi T, Nakahama K;
 XX WPI: 2000-182705/16.
 DR N-PSDB; AA295234.
 XX New phosphodiesterase V useful for screening potential
 PT phosphodiesterase inhibitors for treatment of hypertensive and allergic
 PT diseases.
 XX

XX	Homo sapiens.
OS	
XX	JF2000095759-A.
PX	
XX	04-APR-2000.
PD	
XX	19-JUL-1999; 99JP-0204103.
PF	
XX	21-JUL-1998; 98JP-0204963.
PR	
XX	(TAKE) TAKEDA CHEM IND LTD.
PA	
XX	WPI; 2000-353412/31.
DR	N-PSDB; AAA39042.
DR	
PT	Tricyclic compounds having cyclic GMP-specific phosphodiesterase
XX	inhibitory action useful as pharmaceuticals, and preparation and agents
PT	thereof -
XX	
XX	Example 117; Page 66-68; 71pp; Japanese.
PS	
XX	The present invention describes cyclic GMP (cGMP)-specific
CC	phosphodiesterase inhibitors comprising tricyclic compounds or their
CC	salts. The inhibitors are useful for the treatment and prevention of
CC	erectile failure and feminine function failure. The compounds have
CC	excellent cGMP-phosphodiesterase inhibitory action. The present
CC	sequence represents human cGMP phosphodiesterase V, which is used in
CC	an example from the present invention.
XX	
XX	Sequence 833 AA;
SQ	
	Query Match 38.9%; Score 1366.5; DB 21; Length 833;
	. Best Local Similarity 43.1%; Pred. No. 1.le-112;
	Matches: 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;
QY	54 KRRFNDEIDKLTGYTKSLCMLPIRSDDGEIGVQAQAIN-KIPEGAPFTTDEDKVMQMY 112
Db	: : : : : : : : : :
Db	EDPFRNAEVDIOITGYKTQSILCMPIKNHREVVGVQAQINKSGNGGTTEKDEKFAAY 264
QY	113 LPCGTAISNAQLFAASRKKEYERSRALLEVNDLFEOTDLEKIVKKIMHRAQTLLKCE 172
Db	: : : : : : : : : :
Db	265 LAFCGIVLHAUQYETSLLENKRNOVLLDLASLIFEQQSLEVLILKTAATYIISPQVO 324
QY	173 CSVLLLEDIESPVVKFTKSFELMSPKCSADAENSK-----ESMEKSSYSDWL---- 220
Db	: : : : : : : : : :
Db	325 CTTFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 361
QY	221 ---INNSIAELASTGLPVNISDAYQDPFDAEQDISGFH---IRSVLCVPIMN-SNHQ 273
Db	: : : : : : : : : :
Db	362 ANKINYMAQYVKNMTPEPLNPDYKSKDKRPWTNTGNVNOQCIRSLCLTPIKNGKKNK 421
QY	274 IIGVAQVNLBDG-----KFPDDADQRLEAFVIFCGLGIGNTTIMYDOVKKSWAKOSVAL 328
Db	: : : : : : : : : :
Db	422 VIGVCQLVNKMEENTGVKPKPNRDEQFLFAFVIFCGLGIGINTOMYEAVERAMAKQMVT 481
QY	329 DVLVSYHATCSK--AEVDKFKAAANIPLVSELAIDDHFDDFSLDVDAMITAALRMFMELG 385
Db	: : : : : : : : : :
Db	482 EVLSYHASAEEETRELQSLAAAAPPQAOTLKITDFDSFDELSDLTALCTIRNFDTLN 541
QY	386 MVQKFRTDYETLCRWLLTVRNKYRM-VLYHNWRHAFNVQUMFAMLTATAGFDILTVEYI 444
Db	: : : : : : : : : :
Db	542 LVQNFMQHEVLCRWILLSVKKNYRKNVAYHNWHAFNTAQCMFAALKAGKIQNKLTGLEI 601
QY	445 LAVLVGCGLDHDRHGNTNNAFAQKSGSALAOLYTSTALEHHHFNHAVMILOSQGHNTFA 504
Db	: : : : : : : : : :
Db	602 LALLIALSHDLDRHGYNNSYIORSEHPLAOLY-CHSTMHHFFDOCLMILNSPGNQILS 660
QY	505 NLSKSEYSDLMOLLKQSILATDTLTYPERTERFEFFELYSKGEDYDNKIHNRDIFRSMMLTA 564
Db	: : : : : : : : : :
Db	661 GLSITEEYTKTKIIKQAILATDUALYIKRRGEFFELTRKNGFNLEDDPHQKELFAMLMLTA 720
QY	565 CDLGAVTKPWEISRQVAELVTSEFFEOGDRELERLEKLTPSPAIFDRNRKDELPRLOLEWID 624

Db 721 C D L S A I T K P W I Q O R I A E L V A T E F F D Q D R E R K E L N I E P T D L M N R E K K N I P S M Q V G F I D 780
QY 625 S I C M P L Y Q A L V K V N Y K L K P M L D S V A T N R S K W E E L - - H O K R L L A S T A S S S 672
Db 781 A I C L Q Y E A L T H V S E D C F P L D G C R K N R O K W Q A L A E Q O E K M L I N G E S G Q A 830

Search completed: June 13, 2003, 15:47:18
Job time : 62.4282 secs

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:49:06 ; Search time 13.9203 Seconds
(without alignments)
1490.031 Million cell updates/sec

Title: US-09-663-542-1_COPY_1_194

Perfect score: 975
Sequence: 1 MLKQARRPLFRNVLSTATQWK.....VLLIEDIESPVVFKTSFEL 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	684	10	US-09-891-216-14
2	709	72.7	934	10	US-09-891-216-12
3	709	72.7	934	10	US-09-891-216-15
4	665.5	68.3	142	10	US-09-891-216-5
5	665.5	68.3	142	10	US-09-891-216-17
6	429	44.0	576	10	US-09-891-216-13
7	377	38.7	134	10	US-09-891-216-2
8	377	38.7	134	10	US-09-891-216-16
9	308.5	31.6	833	10	US-09-891-216-3
10	307.5	31.5	875	9	US-10-115-515-10
11	307.5	31.5	875	9	US-10-115-515-23
12	307.5	31.5	875	9	US-10-094-168B-5
13	186	19.1	367	9	US-10-094-168B-3
14	186	19.1	490	9	US-10-094-168B-1
15	165	16.9	779	10	US-09-420-190-1
16	165	16.9	789	10	US-09-321-801-2
17	165	16.9	791	10	US-09-321-801-4
18	165	16.9	796	10	US-09-321-801-15
19	162	16.6	905	12	US-10-094-989-4

20	162	16.6	920	12	US-10-094-989-2	Sequence 2, Appli
21	162	16.6	941	10	US-09-883-825-45	Sequence 45, Appl
22	160	16.4	300	10	US-09-321-801-13	Sequence 13, Appl
23	155.5	15.9	773	9	US-10-202-107-2	Sequence 2, Appli
24	154	15.8	921	10	US-09-883-825-39	Sequence 39, Appl
25	154	15.8	921	12	US-10-094-989-5	Sequence 5, Appli
26	154	15.8	942	10	US-09-883-825-43	Sequence 43, Appl
27	137	14.1	178	10	US-09-321-801-19	Sequence 19, Appl
28	92.5	9.5	1018	9	US-10-101-464A-909	Sequence 909, App
29	92	9.4	51	10	US-09-864-761-40569	Sequence 40569, A
30	80	8.2	499	10	US-09-883-080-2	Sequence 2, Appli
31	78.5	8.1	348	10	US-09-864-761-37615	Sequence 37615, A
32	78.5	8.1	439	9	US-09-056-019-37	Sequence 33, Appl
33	78	8.0	435	10	US-09-866-582-33	Sequence 2, Appli
34	78	8.0	600	10	US-09-975-901-2	Sequence 7, Appli
35	78	8.0	830	9	US-10-033-245-7	Sequence 7, Appli
36	78	8.0	830	9	US-10-033-223-7	Sequence 7, Appli
37	78	8.0	830	9	US-10-033-167-7	Sequence 7, Appli
38	78	8.0	830	9	US-10-033-244-7	Sequence 7, Appli
39	78	8.0	830	9	US-10-033-435-7	Sequence 7, Appli
40	78	8.0	830	9	US-10-032-990-7	Sequence 7, Appli
41	78	8.0	830	9	US-10-032-996-7	Sequence 7, Appli
42	78	8.0	830	9	US-10-033-396-7	Sequence 7, Appli
43	78	8.0	830	12	US-10-033-246-7	Sequence 7, Appli
44	78	8.0	830	12	US-10-033-301-7	Sequence 7, Appli
45	78	8.0	830	12	US-10-033-326-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-891-216-14
; Sequence 14, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 684
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-14

Query Match	100.0%	Score	975;	DB	10;	Length	684;
Best Local Similarity	100.0%	Pred. No.	1.2e-90;				
Matches	194;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MLKQARRPLFRNVLSTATQWKVITRLVQISGASLAEOKEKHODFLIQRQTKTKDRRFND	60				
Db	1	MLKQARRPLFRNVLSTATQWKVITRLVQISGASLAEOKEKHODFLIQRQTKTKDRRFND	60				
QY	61	EIDKLTGYTKSLLCMPIRSSDGEITIGVAQAINKIPEGAPFTTDEDEKVMQWMLPFCGIAI	120				
Db	61	EIDKLTGYTKSLLCMPIRSSDGEITIGVAQAINKIPEGAPFTTDEDEKVMQWMLPFCGIAI	120				
QY	121	SNAAQFAASRKEVERSRALLEVVNDLFEQOTLEKIVKKIMHRAOTLLKRCRCSVLLLED	180				
Db	121	SNAAQFAASRKEVERSRALLEVVNDLFEQOTLEKIVKKIMHRAOTLLKRCRCSVLLLED	180				
QY	181	IESPVVFKTSFEL	194				

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Db      181 IESPVVKTKSFEL 194
|||||
RESULT 2
US-09-891-216-12
; Sequence 12, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-12

Query Match      72.7%; Score 709; DB 10; Length 934;
Best Local Similarity 99.3%; Pred. No. 2.1e-63;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      54 KDRRENDEIDKLTGYKTKSLLCMPITRSSDGETIGVAAQAINKIPEGAPTEDEKVMQYL 113
      :|||||
Db      304 QDRRENDEIDKLTGYKTKSLLCMPITRSSDGETIGVAAQAINKIPEGAPTEDEKVMQYL 363
      :|||||

Qy      114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
      :|||||
Db      364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 423
      :|||||

Qy      174 SVLLEDIESPVVKTKSFEL 194
      :|||||
Db      424 SVLLEDIESPVVKTKSFEL 444
      :|||||

US-09-891-216-5
; Sequence 5, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-5

Query Match      68.3%; Score 665.5; DB 10; Length 142;
Best Local Similarity 95.0%; Pred. No. 4.2e-60;
Matches 133; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy      55 DRRENDEIDKLTGYKTKSLLCMPITRSSDGETIGVAAQAINKIPEGAPTEDEKVMQYLP 114
      :|||||
Db      1 DRRENDEIDKLTGYKTKSLLCMPITRSSDGETIGVAAQAINKIPEGAPTEDEKVMQYLP 60
      :|||||

Qy      115 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 174
      :|||||
Db      61 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 120
      :|||||

Qy      175 VLLLEDIESPVVKTKSFEL 194
      :|||||
Db      121 VLLLEDIESPVVKTKSFEL 139
      :|||||

US-09-891-216-17
; Sequence 17, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-15

Query Match      72.7%; Score 709; DB 10; Length 934;
Best Local Similarity 99.3%; Pred. No. 2.1e-63;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      54 KDRRENDEIDKLTGYKTKSLLCMPITRSSDGETIGVAAQAINKIPEGAPTEDEKVMQYL 113
      :|||||
Db      304 QDRRENDEIDKLTGYKTKSLLCMPITRSSDGETIGVAAQAINKIPEGAPTEDEKVMQYL 363
      :|||||

Qy      114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
      :|||||
Db      364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 423
      :|||||

Qy      174 SVLLEDIESPVVKTKSFEL 194
      :|||||
Db      424 SVLLEDIESPVVKTKSFEL 444
      :|||||

US-09-891-216-15
; Sequence 15, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-15

Query Match      72.7%; Score 709; DB 10; Length 934;
Best Local Similarity 99.3%; Pred. No. 2.1e-63;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```

; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; -09-891-216-17

Query Match      68.3%; Score 665.5; DB 10; Length 142;
Best Local Similarity 95.0%; pred. No. 4.2e-60;
Matches 133; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy      55  DRFNDRIDKLTGYKTKSLLCMPTRSSDGEIIGVAAQAINKIPEGAPFTEDEKVMQMYLP 114
          |||||||
Db      1  DRFNDRIDKLTGYKTKSLLCMPTRSSDGEIIGVAAQAINKIPEGAPFTEDEKVMQMYLP 60
          |||||||

Qy      115 FCGIAISNAQLFAASRREYERSRALLEVNDLFEQDTLEKIVKIMHRAOTLLKRCRCS 174
          |||||||
Db      61  FCGIAISNAQLFAASRREYERSRALLEVNDLFEQDTLEKIVKIMHRAOTLLKRCRCS 120
          |||||||

Qy      175 VLLLEDIESPVVKTKSFEL 194
          |||||||
Db      121 VLLLEDIESP-VSYLLSFKV 139
          |||:

```

```

RESULT 6
US-09-891-216-13
; Sequence 13, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213, 998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293, 221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-13

```

```
. Query Match      44.0% Score 429; DB 10; Length 576;
Best Local Similarity 100.0%; Pred. No. 3.le-35;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps -0
```

Qy	109	MQMYLPCGGTAISNAQLFAASRKKEYRSRALLEVVDLFEEQTDLKIVKKIMHRAQTLL	168
Db	1	MQMYLPCGGTAISNAQLFAASRKKEYRSRALLEVVDLFEEQTDLKIVKKIMHRAQTLL	60
Qy	169	KCERCSVLLLEDIESPVVKFTKSPEL	194
Db	61	KCERCSVLLLEDIESPVVKFTKSPEL	86

```

RESULT 7
US-09-891-216-2
: Sequence 2, Application US/09891216
: Patent No. US20020103120A1
: GENERAL INFORMATION:
: APPLICANT: Ramakrishnan, Shyam
: TITLE OF INVENTION: Regulation of Human
: TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
: FILE REFERENCE: 02973.00511

```

```

; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/2213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(134)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-891-216-2

```

Query Match	38.7%	Score 377;	DB 10;	Length 134;
Best Local Similarity	68.9%	Pred. No. 8.3e-31;		
Matches	82;	Conservative 3;	Mismatches 4;	Indels 30; Gaps 2;
Qy	105	DEKVMQMYLFPFCGIATISNAQLFAASRKEYERSR-----	137	
Db	3	DNKVMQMYLFPFCGIATISNAQLFAASRKEYERSRVSYRDVYLVKMSQVXPRTCFFLIVRKS	62	
Qy	138	--ALLEVVNDLFPQDTLDKIVKIMHRAQTLLKCRCSVLLLEDIESPVVVKFTKSEEL	194	
Db	63	CFALLEVVNDLFPQDTLDKIVKIMHRAQTLLKCRCSVLLLEDIESP-VSYLLSPKV	120	

```

RESULT 8
US-09-891-216-16
; Sequence 16, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891.216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 134
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(134)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-891-216-16

```

	Query Match	38.7%	Score 377:	DB 10:	Length 134:
	Best Local Similarity	68.9%	Pred. No. 8.3e-31:		
	Matches 82:	Conservative	3:	Mismatches 4:	Indels 30: Gaps 2:
Qy	105	DEKVMQYLPFCGIAISNAOLFASRKEYERSR-----	137		
Db	3	DNKVMQYLPFCGIAISNAOLFASRKEYERSR	62		
Qy	138	--ALLEVNDLFEOTDLEIKVIMHRAOTLLKCRCSVLLEDIESPVVFKTSP	194		
Db	63	CFALLEVNDLFEOTDLEIKVIMHRAOTLLKCRCSVLLEDIESP--VSYLLSPK	120		

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A1
US-10-094-168B-1

Query Match 19.1%; Score 186; DB 9; Length 490;
Best Local Similarity 29.7%; Pred. No. 1.2e-10;
Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;
QY 34 SLAEKQEK-HQDFLIQQT------KDRFNDEIDKLTGYTKSLLCM 76
Db 12 SFKSEMEKSSYSDMLNNSIAELVASTGLPVNISDAYQDPFDAEQISGFHRSVLCV 71
QY 77 PIRSDGEIIGVAQAINKIPGAPFTEDEKVMQMYLPFCGIAISNAOLFASRKEYERS 136
Db 72 PIWNSNHOIIGVAQVNLNL-DGKPFDDADQRIFEAFVIFCGLGINNNTIMYDQVKSWAKQ 130
QY 137 RALLEVN 144
Db 131 SVALDVLS 138

RESULT 15
US-09-420-190-1
; Sequence 1, Application US/09420190
; Patent No. US20020081633A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide Phosphodiesterase
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-420-190-1

Query Match 16.9%; Score 165; DB 10; Length 779;
Best Local Similarity 45.8%; Pred. No. 3.2e-08;
Matches 33; Conservative 15; Mismatches 22; Indels 2; Gaps 2;
QY 55 DRRFNDEIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPGAPFTEDEKVMQMYLP 114
Db 349 DPRENREVDLYTGYTRNLCMPI-VSRGSVIGVQMVNKI-SGSAFSKTDENNFKMFAY 406
QY 115 FCGIAISNAQLF 126
Db 407 FCALALHCANNY 418

Search completed: June 13, 2003, 15:59:22
Job time : 14.9203 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:38:09 ; Search time 16.5718 Seconds
(without alignments)
1559.921 Million cell updates/sec

Title: US-09-663-542-1_COPY_1_194

Perfect score: 975

Sequence: 1 MLKQARRPLFRNLSATQWK.....VLLIEDIESPVVKFTKSFEL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SID22/qcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/qcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/qcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	100.0	684	22	Human type 11 phos
2	975	100.0	684	22	Human cyclic nucle
3	882	90.5	685	22	Rat type 11 phosph
4	709	72.7	934	22	Human type 11 phos
5	705	72.3	935	22	Rat type 11 phosph
6	665.5	68.3	142	23	Human phosphodiester
7	429	44.0	576	22	Amino acid sequenc
8	376.5	38.6	135	23	Human phosphodiester
9	354.5	36.4	1232	22	Human phosphodiester
10	349	35.8	1284	22	Drosophila melanog

11	349	35.8	1284	23	ABB08376	D. melanogaster CG
12	307.5	31.5	494	19	AAW42013	cGMP-binding phosph
13	307.5	31.5	549	19	AAW42014	cGMP-binding phosph
14	307.5	31.5	832	21	AAW78939	Human phosphodiester
15	307.5	31.5	832	21	AAW78940	Human phosphodiester
16	307.5	31.5	833	21	AAW90912	Human cGMP phospho
17	307.5	31.5	833	22	AAW97024	Human phosphodiester
18	307.5	31.5	875	16	AAW66565	Cyclic guanosine m
19	307.5	31.5	875	19	AAW42011	Bovine cGMP-binding
20	307.5	31.5	875	20	AAW14990	Bovine cGMP-binding
21	307.5	31.5	875	20	AAW14991	Human cGMP-binding
22	307.5	31.5	1126	21	AAW84879	Amino acid sequenc
23	301.5	30.9	875	16	AAW66564	Cyclic guanosine m
24	203	20.8	930	23	AAU79716	Trypanosoma brucei
25	199	20.4	930	23	AAU79718	Trypanosoma brucei
26	186	19.1	367	21	AAW95522	Human cyclic nucle
27	186	19.1	490	21	AAW95521	Human cyclic nucle
28	182.5	18.7	474	22	AAW67531	Amino acid sequenc
29	165	16.9	135	21	AAW53949	Peptide representi
30	165	16.9	749	21	AAW53959	Formula III repres
31	165	16.9	750	21	AAW53960	Formula IV repres
32	165	16.9	754	21	AAW53961	Formula V repres
33	165	16.9	758	21	AAW53962	Formula VI repres
34	165	16.9	759	21	AAW53972	Amino acid sequenc
35	165	16.9	766	20	AAW13934	Human phosphodiester
36	165	16.9	766	22	AAW28256	Human phosphodiester
37	165	16.9	767	21	AAW53963	Formula VII repres
38	165	16.9	774	21	AAW57306	Rat phosphodiester
39	165	16.9	779	20	AAW13936	Human phosphodiester
40	165	16.9	779	21	AAW26853	Human phosphodiester
41	165	16.9	779	22	AAW73486	Human cyclic nucle
42	165	16.9	779	22	AAW28258	Human phosphodiester
43	165	16.9	788	21	AAW26856	Human phosphodiester
44	165	16.9	789	21	AAW26854	Human phosphodiester
45	165	16.9	789	21	AAW53935	A human phosphodi

ALIGNMENTS

RESULT 1
AAG62678
ID AAG62678 standard; Protein; 684 AA.
AC AAG62678;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human type 11 phosphodiesterase SBQ ID NO: 4.
XX
KW Human: type 11 phosphodiesterase; PDE11; signal transduction;
KW selective inhibition.
XX
OS Homo sapiens.
XX
PN WO200146436-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-JP09118.
XX
PR 22-DEC-1999; 99JP-0364866.
PR 01-JUN-2000; 2000JP-0163875.
XX
XX (TANA) TANABE SEIYAKU CO.
XX
XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX
XX WPI; 2001-418074/44.
XX
XX N-PSDB; AAH46709;
XX
XX Type 11 phosphodiesterases and encoded genes with activity of
XX hydrolyzing cyclic nucleotides, useful for studying intracellular

PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy

PS Claim 2; Page 49-51; 77pp; Japanese.

XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.

XX Sequence 684 AA;

Query Match 100.0%; Score 975; DB 22; Length 684;
Best Local Similarity 100.0%; Pred. No. 5.5e-96;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKQARRPLFRNVL SATQWKVKITRLVQISGASLAEKQKHQDFLQRTKTKDRRND 60
Db 1 MKQARRPLFRNVL SATQWKVKITRLVQISGASLAEKQKHQDFLQRTKTKDRRND 60
Qy 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGIAI 120
Db 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGIAI 120
Qy 121 SNAOLFASRKEYERSRALLVNDLFEEQTDLEKIVKIMHRAQTLLKCERC SVLLLED 180
Db 121 SNAOLFASRKEYERSRALLVNDLFEEQTDLEKIVKIMHRAQTLLKCERC SVLLLED 180
Qy 181 IESPVVKFTKSFEL 194
Db 181 IESPVVKFTKSFEL 194

RESULT 2

AAB35472
ID AAB35472 standard; protein: 684 AA.

XX AC AAB35472;

XX DT 06-JUN-2001 (first entry)

XX Human cyclic nucleotide phosphodiesterase PDEXV.

XX Human; cyclic nucleotide phosphodiesterase; PDEXV; sexual dysfunction;
KW cardiovascular disease; gastrointestinal disorder; corpus cavernosum;
KW kidney; liver; skeletal muscle; testis prostate; spleen.

XX OS Homo sapiens.

XX PN EP1085089-A2.

XX PD 21-MAR-2001.

XX PF 14-SEP-2000; 2000EP-0307981.

XX PR 17-SEP-1999; 99GB-0022124.

XX PA (PFIZ) PFIZER LTD.

XX PA (PFIZ) PFIZER INC.

XX PI Fidock MD, Robas NM;

XX WPI; 2001-246900/26.

XX DR N-PSDB; AAF62311.

XX Human cyclic nucleotide phosphodiesterase and its nucleotide sequence
PT useful for treating cardiovascular disorders, sexual dysfunction and
PT screening for drugs to treat associated disorders

PS Claim 1; Page 37-41; 44pp; English.

XX

CC The present invention describes the protein and coding sequences of the
CC human cyclic nucleotide phosphodiesterase PDEXV. This enzyme is capable
CC of catalysing the degradation of cyclic nucleotides. The sequences are
CC useful in the treatment of cardiovascular, gastrointestinal, spleen,
CC corpus cavernosum, kidney, liver, skeletal muscle, testis and prostate
CC related disorders, and in the enhancement of the male erectile response
CC and the treatment of female sexual dysfunction. The present sequence is
CC the PDEXV protein.

XX Sequence 684 AA;

Query Match 100.0%; Score 975; DB 22; Length 684;
Best Local Similarity 100.0%; Pred. No. 5.5e-96;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKQARRPLFRNVL SATQWKVKITRLVQISGASLAEKQKHQDFLQRTKTKDRRND 60

Db 1 MKQARRPLFRNVL SATQWKVKITRLVQISGASLAEKQKHQDFLQRTKTKDRRND 60

Qy 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGIAI 120

Db 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGIAI 120

Qy 121 SNAOLFASRKEYERSRALLVNDLFEEQTDLEKIVKIMHRAQTLLKCERC SVLLLED 180

Db 121 SNAOLFASRKEYERSRALLVNDLFEEQTDLEKIVKIMHRAQTLLKCERC SVLLLED 180

Qy 181 IESPVVKFTKSFEL 194

Db 181 IESPVVKFTKSFEL 194

RESULT 3

AAG62679
ID AAG62679 standard; Protein: 685 AA.

XX AC AAG62679;

XX DT 19-SEP-2001 (first entry)

XX Rat type 11 phosphodiesterase SEQ ID NO: 6.

XX Rat; type 11 phosphodiesterase; PDE11; signal transduction;
KW selective inhibition.

XX OS Rattus sp.

XX WO200146436-A1.

XX PD 28-JUN-2001.

XX PF 22-DEC-2000; 2000WO-JP09118.

XX PR 22-DEC-1999; 99JP-0364866.

XX PR 01-JUN-2000; 2000JP-0163875.

XX PA (TANA) TANABE SEIYAKU CO.

XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;

XX WPI; 2001-418074/44.

XX DR N-PSDB; AAH46710.

XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy

XX Claim 2; Page 55-57; 77pp; Japanese.

XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for

CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.

XX Sequence 685 AA;

Query Match 90.5%; Score 882; DB 22; Length 685;
Best Local Similarity 90.7%; Pred. No. 5.7e-86;
Matches 176; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1' MLQARRPLFNVL SATQKKVKTIRLVQISGASLAERKHQDFLQRFQTKTKDRRND 60
DB 1 MLQARRSFNVRVSATQWRKVGSTROGQISGAFLAERLDKHQDFLTRMTRTKDRRND 60
QY 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGTAI 120
DB 61 EIDKLTGYKTKSLLCMPIRNSDGEIIGVAQAINKYPEGAPTEDEKVMQMYLPFCGTAI 120
QY 121 SNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC SVLLLED 180
DB 121 SNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC SVLLLED 180
QY 181 IESPVVKETKSFEL 194
DB 181 IESPVVKETKSFEL 194

RESULT 4

AAG62677
ID AAG62677 standard; Protein; 934 AA.

XX AC AAG62677;

XX DT 19-SEP-2001 (first entry)

XX DE Human type 11 phosphodiesterase SEQ ID NO: 2.

XX DE Human; type 11 phosphodiesterase; PDE11; signal transduction;
KW selective inhibition.

XX OS Homo sapiens.

XX PN WO200146436-A1.

XX PD 28-JUN-2001.

XX PF 22-DEC-2000; 2000WO-JP09118.

XX PR 22-DEC-1999; 99JP-0364866.

XX PR 01-JUN-2000; 2000JP-0163875.

XX PA (TANA) TANABE SEIYAKU CO.

XX PI Omori K, Yuasa K, Kotera J, Oda K, Michibata H;

XX DR WPI; 2001-418074/44.

XX DR N-PSDB; AAH46708.

XX XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy .

PS Claim 2; Page 42-45; 77pp; Japanese.

XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present

CC sequence is a protein of the invention.

XX Sequence 934 AA;

Query Match 72.7%; Score 709; DB 22; Length 934;
Best Local Similarity 99.3%; Pred. No. 3.7e-67;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 54 KDRFNDKIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYL 113
DB 304 QDRFNDKIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYL 363
QY 114 PFCGTAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
DB 364 PFCGTAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 423
QY 174 SVLLLEDIESPVVKETKSFEL 194
DB 424 SVLLLEDIESPVVKETKSFEL 444

RESULT 5

AAG62680

ID AAG62680 standard; Protein; 935 AA.

XX AC AAG62680;

XX DT 19-SEP-2001 (first entry)

XX DE Rat type 11 phosphodiesterase SEQ ID NO: 39.

XX DE Rat; type 11 phosphodiesterase; PDE11; signal transduction;
KW selective inhibition.

XX OS Rattus sp.

XX PN WO200146436-A1.

XX PD 28-JUN-2001.

XX PF 22-DEC-2000; 2000WO-JP09118.

XX PR 22-DEC-1999; 99JP-0364866.

XX PR 01-JUN-2000; 2000JP-0163875.

XX PA (TANA) TANABE SEIYAKU CO.

XX PI Omori K, Yuasa K, Kotera J, Oda K, Michibata H;

XX DR WPI; 2001-418074/44.

XX DR N-PSDB; AAH46742.

XX XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy .

PS Claim 2; Page 69-72; 77pp; Japanese.

XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.

XX Sequence 935 AA;

Query Match 72.3%; Score 705; DB 22; Length 935;
Best Local Similarity 97.9%; Pred. No. 9.9e-67;
Matches 138; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 54 KDRFNDEIDKLTGYKTKSLCMLPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQYL 113
 :|||||
 Db 304 QDRFNDEIDKLTGYKTKSLCMLPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQYL 363
 :|||||

QY 114 PFCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCERC 173
 :|||||
 Db 364 PFCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCERC 423
 :|||||

QY 174 SVLLEDIESPVVFKTSFEL 194
 :|||||
 Db 424 SVLLEDIESPVVFKTSFEL 444
 :|||||

RESULT 6
 AAE17789
 ID AAE17789 standard; Protein; 142 AA.
 XX
 AC AAE17789;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human phosphodiesterase (PDE)-like enzyme #2.
 XX
 KW Human; phosphodiesterase; PDE-like enzyme; benign prostate hyperplasia;
 KW urinary incontinence; erectile dysfunction; cardiovascular disorder;
 KW cancer; diabetes; ischaemic disease; myocardial infarction; cytostatic;
 KW vasodilator; cardiant.
 XX
 OS Homo sapiens.
 XX
 PN WO200200854-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001WO-EP07289.
 XX
 PR 26-JUN-2000; 2000US-213998P.
 PR 25-MAY-2001; 2001US-293221P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Ramakrishnan S;
 XX
 DR WPI; 2002-090522/12.
 DR N-PSDB; AAD28571.
 XX

Isolated polynucleotide encoding a human phosphodiesterase-like enzyme,
 useful for treating a disease such as urinary incontinence, benign
 prostate hyperplasia, erectile dysfunction, diabetes, cancer or
 cardiovascular disorder.

Claim 25; Fig 5; 165pp; English.

The present invention relates to human phosphodiesterase (PDE)-like
 enzymes and their corresponding polynucleotides. The invention also
 relates to reagents which regulate PDE-like enzyme activity and reagents
 which bind to human PDE-like enzyme gene products which can be used to
 regulate degradation of cGMP. Sequences of the invention are useful for
 modulating the activity of a PDE-like enzyme in a disease such as urinary
 incontinence, benign prostate hyperplasia, erectile dysfunction, cancer,
 diabetes or cardiovascular disorder (e.g. ischaemic diseases, myocardial
 infarction). The present sequence is human PDE-like enzyme.

XX
 SQ Sequence 142 AA;
 Query Match 68.3%; Score 665.5; DB 23; Length 142;
 Best Local Similarity 95.0%; Pred. No. 1.3e-63;
 Matches 133; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 55 DRFNDEIDKLTGYKTKSLCMLPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQYLP 114
 :|||||
 Db 1 DRFNDEIDKLTGYKTKSLCMLPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQYLP 60
 :|||||

QY 115 FCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCERC 174
 :|||||
 Db 61 FCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCERC 120
 :|||||

QY 175 VLLLEDIESPVVFKTSFEL 194
 :|||||
 Db 121 VLLLEDIESP-VSYLLSPKV 139
 :|||||

RESULT 7
 AAG67533
 ID AAG67533 standard; Protein; 576 AA.
 XX
 AC AAG67533;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of a human phosphodiesterase polypeptide.
 XX
 KW Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension;
 KW nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism;
 KW osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis;
 KW Parkinson's disease; dementia; infectious disease; malignant tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200166716-A1.
 XX
 PD 13-SEP-2001.
 XX
 PF 06-MAR-2001; 2001WO-JP01720.
 XX
 PR 07-MAR-2000; 2000JP-0061464.
 PR 10-JUL-2000; 2000JP-0208610.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Miyaji H, Haruoka M, Ota T, Kawabata A, Sugano S, Nakamura Y;
 XX
 DR WPI; 2001-570769/64.
 DR N-PSDB; AAH78232.
 XX

Polypeptides with phosphodiesterase activity and DNA for treatment of
 diabetes, ischemic heart disease, hypertension, nephritis,
 pancreatitis, ulcers, allergies, asthma

Claim 1; Page 90-93; 105pp; Japanese.

The present sequence encodes a human polypeptide which has
 phosphodiesterase activity. The phosphodiesterase polypeptide and
 polynucleotide are used for the treatment and prevention of diabetes,
 ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers,
 allergies, asthma, rheumatism, osteoporosis, pain, anxiety,
 schizophrenia, manic depressive psychosis, Parkinson's disease,
 dementia, infectious diseases, and malignant tumours.

XX
 SQ Sequence 576 AA;
 Query Match 44.0%; Score 429; DB 22; Length 576;
 Best Local Similarity 100.0%; Pred. No. 2.7e-37;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MQMVLPCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLL 168
 :|||||
 Db 1 MQMVLPCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLL 60
 :|||||

QY 169 KCERCSVLLLEDIESPVVFKTSFEL 194
 :|||||
 Db 61 KCERCSVLLLEDIESPVVFKTSFEL 86
 :|||||

RESULT 8
 AAE17789

Db 382 AQLYKSOLEIKRNOVLDMARMIFEOSTIEHMFVRIILTHMQSLIOQORVILLVHEAD 441
Oy 183 SPVVKFTKSFE 193
Db 442 KG--SFSRVFD 450

RESULT 12
AAW42013
ID AAW42013 standard; protein; 494 AA.
AC AAW42013;
XX 28-MAY-1998 (first entry)
DE CGMP-binding phosphodiesterase fragment 2.
XX Human cGMP-binding phosphodiesterase; cGB-PDE; control sequence;
KW antibody.
XX Homo sapiens.
OS US5702936-A.
PN 30-DEC-1997.
XX 27-MAY-1994; 94US-0250847.
PF 27-MAY-1994; 94US-0250847.
PR 27-MAY-1993; 93US-0068051.
XX (ICOS-) ICOS CORP.
PA (UYVA-) UNIV VANDERBILT.
PA (UNIW) UNIV WASHINGTON.
XX Beavo JA, Corbin JD, Ferguson KM, Francis SH, Kadlecsek A;
PI Loughney K, McAllister-Lucas LM, Sonnenburg WK, Thomas MK;
XX WPI; 1998-076421/07.
XX Fragments of human cGMP-binding phosphodiesterase - used for
PT isolating modulators of cGB-PDE associated diseases
XX Claim 2; Pages -: 42pp; English.

This sequence is a fragment of the human cGMP-binding phosphodiesterase (cGB-PDE), consisting of amino acid residues 1-494. The novel polypeptide can be used for the detection of cGB-PDE and the isolation of its expression control sequences. It can also be used to identify genetic alterations in the cGB-PDE locus associated with diseases. Antibodies specific for cGB-PDE fragments can also be used in detecting and quantifying the amount of cGB-PDE present in samples. (Note: this sequence is not given in the specification but is generated from the defined wild type sequence).

Query Match 31.5%; Score 307.5; DB 19; Length 494;
Best Local Similarity 46.1%; Pred. No. 2.6e-24;
Matches 59; Conservative 31; Mismatches 27; Indels 1; Gaps 1;
Sequence 494 AA:

Oy 54 KDRFNDEIDKLTGYKTKSLLCMPTRSSDGEIIGVQAQAIN-KIPEGAPFTEDEKVMQY 112
Db 247 EDPRENAEVDQITGYKTSILCMPIKNHREEVGVQAQAINKSGNGTFTKEDKDFRAY 306
Oy 113 LPFGCIATSNALQFAASRKEYERSRALLEVVDLFEEOITDLEKIVKIMHRAQTLLKCR 172
Db 307 LAFCGIVLHNAQLYETSLENKRNQVLLDASLIFEEOQSLEVLILKTAATIIISPMQVOK 366
Oy 173 CSQLLED 180
Db 367 CTIFIVDE 374

RESULT 13
AAW42014
ID AAW42014 standard; protein; 549 AA.
XX AC AAW42014;
XX 28-MAY-1998 (first entry)
DE CGMP-binding phosphodiesterase fragment 3.
XX Human cGMP-binding phosphodiesterase; cGB-PDE; control sequence;
KW antibody.
XX Homo sapiens.
OS US5702936-A.
PN 30-DEC-1997.
XX 27-MAY-1994; 94US-0250847.
PF 27-MAY-1994; 94US-0250847.
PR 27-MAY-1993; 93US-0068051.
XX (ICOS-) ICOS CORP.
PA (UYVA-) UNIV VANDERBILT.
PA (UNIW) UNIV WASHINGTON.
XX Beavo JA, Corbin JD, Ferguson KM, Francis SH, Kadlecsek A;
PI Loughney K, McAllister-Lucas LM, Sonnenburg WK, Thomas MK;
XX WPI; 1998-076421/07.
XX Fragments of human cGMP-binding phosphodiesterase - used for
PT isolating modulators of cGB-PDE associated diseases
XX Claim 3; Pages -: 42pp; English.

This sequence is a fragment of the human cGMP-binding phosphodiesterase (cGB-PDE), consisting of amino acid residues 1-549. The novel polypeptide can be used for the detection of cGB-PDE and the isolation of its expression control sequences. It can also be used to identify genetic alterations in the cGB-PDE locus associated with diseases. Antibodies specific for cGB-PDE fragments can also be used in detecting and quantifying the amount of cGB-PDE present in samples. (Note: this sequence is not given in the specification but is generated from the defined wild type sequence).

Query Match 31.5%; Score 307.5; DB 19; Length 549;
Best Local Similarity 46.1%; Pred. No. 3e-24;
Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;
Sequence 549 AA:

Oy 54 KDRFNDEIDKLTGYKTKSLLCMPTRSSDGEIIGVQAQAIN-KIPEGAPFTEDEKVMQY 112
Db 247 EDPRENAEVDQITGYKTSILCMPIKNHREEVGVQAQAINKSGNGTFTKEDKDFRAY 306
Oy 113 LPFGCIATSNALQFAASRKEYERSRALLEVVDLFEEOITDLEKIVKIMHRAQTLLKCR 172
Db 307 LAFCGIVLHNAQLYETSLENKRNQVLLDASLIFEEOQSLEVLILKTAATIIISPMQVOK 366
Oy 173 CSQLLED 180
Db 367 CTIFIVDE 374

RESULT 14
AAW78939

ID AAY78939 standard; Protein: 832 AA.
XX AC AAY78939;
XX DT 05-JUN-2000 (first entry)
XX DE Human phosphodiesterase V amino acid sequence #1.
XX KW Phosphodiesterase V; human; hypertension; pulmonary hypertension;
KW atherosclerosis, cerebral infarction; allergic rhinitis; kidney failure;
XX KW diabetic complication; glaucoma.
XX OS Homo sapiens.
XX PN WO200005383-A1.
XX PD 03-FEB-2000.
XX PF 19-JUL-1999; 99WO-JP03865;
XX PR 21-JUL-1998; 98JP-0204964.
XX PR 16-APR-1999; 99JP-0108974.
XX PA (TAKE) TAKEDA CHEM IND LTD.
XX PI Tarui N, Doi T, Nakahama K;
XX DR WPI; 2000-182705/16.
XX DR N-PSDB; AAZ95233.
XX PT New phosphodiesterase V useful for screening potential
PT phosphodiesterase inhibitors for treatment of hypertensive and allergic
XX diseases.
XX PS Disclosure: Fig 5-6; 96pp; Japanese.
XX CC This sequence represents a human phosphodiesterase V amino acid sequence.
CC The phosphodiesterase V protein, its fragments and salts are useful in
CC the identification of phosphodiesterase V inhibitors for use in the
CC treatment of hypertension, pulmonary hypertension, atherosclerosis,
CC cerebral infarction, allergic rhinitis, kidney failure, diabetic
CC complications, and glaucoma.
XX SQ Sequence 832 AA;
Query Match 31.5%; Score 307.5; DB 21; Length 832;
Best Local Similarity 46.1%; Pred. No. 5.3e-24;
Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;
QY 54 KDRFNDEIDKLTGYKTKSLCMLPIRSSDGEIIGVAQAIN-KIPEGAPFTTDEDEKVMOMY 112
: | | | | : : : : : | | | | : : : : : | | | | : : : : : | | | | : : : : :
Db 205 EDPRENAEVDQITGYKTSILCMLPIKHNREEVGVGAQAINKKSGNGGTFTEKDEKFAAY 264
QY 113 LPFCGIAISNAQLFAASRKEVERSRALLEVNDLFEETDLEKIVKIMHRAQTLLKGER 172
: | | | | : : : : : | | | | : : : : : | | | | : : : : : | | | | : : : : :
Db 265 LAFCGIVLHNAQLYETSLLENKRNQVLLDLASLIFEEOQSLEVLTKIAATIISFMQVOK 324
QY 173 CSVLLED 180
: : : : :
Db 325 CTIFIVDE 332
RESULT 15
AAY78940
ID AAY78940 standard; Protein: 832 AA.
XX AC AAY78940;
XX DT 05-JUN-2000 (first entry)
XX DE Human phosphodiesterase V amino acid sequence #2.
XX KW Phosphodiesterase V; human; hypertension; pulmonary hypertension;

KW atherosclerosis, cerebral infarction; allergic rhinitis; kidney failure;
XX KW diabetic complication; glaucoma.
XX OS Homo sapiens.
XX PN WO200005383-A1.
XX PD 03-FEB-2000.
XX PF 19-JUL-1999; 99WO-JP03865.
XX PR 21-JUL-1998; 98JP-0204964.
XX PR 16-APR-1999; 99JP-0108974.
XX PA (TAKE) TAKEDA CHEM IND LTD.
XX PI Tarui N, Doi T, Nakahama K;
XX DR WPI; 2000-182705/16.
XX DR N-PSDB; AAZ95233.
XX PT New phosphodiesterase V useful for screening potential
PT phosphodiesterase inhibitors for treatment of hypertensive and allergic
XX diseases.
XX PS Claim 7; Page 88-90; 96pp; Japanese.
XX CC This sequence represents a human phosphodiesterase V amino acid sequence.
CC The phosphodiesterase V protein, its fragments and salts are useful in
CC the identification of phosphodiesterase V inhibitors for use in the
CC treatment of hypertension, pulmonary hypertension, atherosclerosis,
CC cerebral infarction, allergic rhinitis, kidney failure, diabetic
CC complications, and glaucoma.
XX SQ Sequence 832 AA;
Query Match 31.5%; Score 307.5; DB 21; Length 832;
Best Local Similarity 46.1%; Pred. No. 5.3e-24;
Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;
QY 54 KDRFNDEIDKLTGYKTKSLCMLPIRSSDGEIIGVAQAIN-KIPEGAPFTTDEDEKVMOMY 112
: | | | | : : : : : | | | | : : : : : | | | | : : : : : | | | | : : : : :
Db 205 EDPRENAEVDQITGYKTSILCMLPIKHNREEVGVGAQAINKKSGNGGTFTEKDEKFAAY 264
QY 113 LPFCGIAISNAQLFAASRKEVERSRALLEVNDLFEETDLEKIVKIMHRAQTLLKGER 172
: | | | | : : : : : | | | | : : : : : | | | | : : : : : | | | | : : : : :
Db 265 LAFCGIVLHNAQLYETSLLENKRNQVLLDLASLIFEEOQSLEVLTKIAATIISFMQVOK 324
QY 173 CSVLLED 180
: : : : :
Db 325 CTIFIVDE 332
Search completed: June 13, 2003, 15:47:18
Job time : 16.5718 secs

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:44:04 ; Search time 12.8155 Seconds
(without alignments)

3119.127 Million cell updates/sec

Title: US-09-663-542-1_COPY_1_194

Perfect score: 975

Sequence: 1 MLKQARRPLFRNLSATQWK.....VLLLEDIESPVVFKTKSFEL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	100.0	684	4 Q9GZY7	Q9gy7 homo sapien
2	882	90.5	685	11 Q8VID7	Q8vid7 rattus norv
3	813	83.4	988	4 Q96S76	Q96s76 homo sapien
4	709	72.7	934	4 Q9HCR9	Q9hcr9 homo sapien
5	705	72.3	935	11 Q8VID6	Q8vid6 rattus norv
6	433	44.4	581	11 Q8VID8	Q8vid8 rattus norv
7	429	44.0	576	4 Q9HB46	Q9hb46 homo sapien
8	354.5	36.4	1018	5 Q95TW8	Q95tw8 drosophila
9	354.5	36.4	1232	5 Q9VFI9	Q9vfi9 drosophila
10	349	35.8	1284	5 Q9GVJ79	Q9gvj79 drosophila
11	203	20.8	930	5 Q9GQ06	Q9gqu6 trypanosoma
12	201	20.6	836	11 Q8R0D4	Q8rod4 mus musculus
13	201	20.6	861	11 Q91ZQ1	Q91zq1 mus musculus
14	199	20.4	930	5 Q8WQX9	Q8wx9 trypanosoma
15	189.5	19.4	819	5 Q96076	Q96076 ephydatia f
16	186	19.1	490	4 Q9NY45	Q9ny45 homo sapien

17	185	19.0	861	13 Q8UUY5	Q8uuy5 rana pipien
18	183	18.8	692	6 Q97746	Q97746 canis famil
19	183	18.8	856	6 Q9MYV0	Q9myv0 canis famil
20	181.5	18.6	857	13 Q8UUY6	Q8uuy6 rana pipien
21	181.5	18.6	866	13 Q8UUY7	Q8uuy7 rana pipien
22	180	18.5	800	11 Q62037	Q62037 mus musculu
23	178.5	18.3	860	2 P94182	P94182 anabaena sp
24	178.5	18.3	860	16 Q8YVS0	Q8yvs0 anabaena sp
25	174.5	17.9	859	16 P94181	P94181 anabaena sp
26	165	16.9	657	4 Q9NTV4	Q9ntv4 homo sapien
27	165	16.9	714	4 Q9HCP9	Q9hcp9 homo sapien
28	165	16.9	779	11 Q9WV11	Q9wv11 mus musculu
29	165	16.9	788	11 Q9QYJ5	Q9qyj5 rattus norv
30	165	16.9	789	4 Q9ULW9	Q9ulw9 homo sapien
31	165	16.9	794	11 Q9QYJ6	Q9qyj6 rattus norv
32	164.5	16.9	485	5 Q9GTN9	Q9gtn9 trypanosoma
33	129	13.2	944	16 Q8YV44	Q8yv44 anabaena sp
34	118.5	12.2	445	2 Q9FSY4	Q9fsy4 anabaena va
35	118.5	12.2	1245	5 Q96195	Q96195 plasmodium
36	118.5	12.2	1850	16 Q8YVG4	Q8yvg4 anabaena sp
37	117	12.0	101	4 Q9UD49	Q9ud49 homo sapien
38	117	12.0	773	2 Q9XBM4	Q9xbm4 myxococcus
39	116	11.9	1900	16 Q8YN83	Q8yn83 anabaena sp
40	111.5	11.4	573	16 Q53473	Q53473 mycobacteri
41	104	10.7	235	11 Q9QYT5	Q9qyt5 rattus norv
42	95	9.7	1808	16 Q8YZY1	Q8zyz1 anabaena sp
43	94.5	9.7	578	16 P95194	P95194 mycobacteri
44	94	9.6	540	17 Q971R4	Q971r4 sulfolobus
45	94	9.6	1777	16 Q9L708	Q9l708 anabaena sp

ALIGNMENTS

RESULT 1

Q9GZY7	ID	Q9GZY7	PRELIMINARY;	PRT;	684 AA.
AC	Q9GZY7;				
DT	01-MAR-2001	(TEMBLrel. 16, Created)			
DT	01-MAR-2001	(TEMBLrel. 16, Last sequence update)			
DT	01-JUN-2002	(TEMBLrel. 21, Last annotation update)			
DE	CAMP/CGMP cyclic nucleotide phosphodiesterase IIA3 (Phosphodiesterase IIA2).				
DE	IIA2).				
GN	PDE1IA3 OR HSPDE1IA.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RX	SEQUENCE FROM N.A.				
RP	MEDLINE=20524097; PubMed=11050148;				
RA	Hetman J.M., Robas N.M., Baxendale R., Fidock M., Phillips S.C.,				
RA	Soderling S.H., Beavo J.A.;				
RT	"Cloning and characterization of two splice variants of human phosphodiesterase IIA."				
RL	Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=TESTIS;				
RP	MEDLINE=20459516; PubMed=10906126;				
RA	Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;				
RA	"Isolation and Characterization of Two Novel Phosphodiesterase PD1IA				
RT	Variants Showing Unique Structure and Tissue-specific Expression."				
RL	J. Biol. Chem. 275:31469-31479(2000).				
EMBL	AJ278682; CAC15567.1; -				
DR	EMBL; AB038041; BAB16372.1; -				
DR	InterPro; IPR003018; GAF.				
DR	InterPro; IPR003607; ME_Pplase_Hdc.				
DR	InterPro; IPR002073; PDEase.				
DR	Pfam; PF01590; GAF; 2.				
DR	Pfam; PF00233; PDEase; 1.				
DR	PRINTS; PR00387; PDIESTERASE1.				
DR	SMART; SM00065; GAF; 2.				

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DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 684 AA; 78133 MW; 1E41C4F519D9DB1E CRC64;

Query Match 100.0%; Score 975; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 3.8e-74;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKQARRPLFRNVLSATQWKVKITRLVQISGASLAEKQKHQDFLIQRTKTKDRRND 60
DB 1 MLKQARRPLFRNVLSATQWKVKITRLVQISGASLAEKQKHQDFLIQRTKTKDRRND 60
QY 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAI 120
DB 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAI 120
QY 121 SNAQLFAASRKEYERSALLEVNDLFEEQTDLEKIVKIMHRAQTLKRCRCSVLLED 180
DB 121 SNAQLFAASRKEYERSALLEVNDLFEEQTDLEKIVKIMHRAQTLKRCRCSVLLED 180
QY 181 IESPVVKFTKSFEL 194
DB 181 IESPVVKFTKSFEL 194

RESULT 2
Q8VID7 PRELIMINARY; PRT; 685 AA.
AC Q8VID7
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A3.
GN RNPDE11A3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohguru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
(pDE11A): comparison of rat and human pDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL; AB059361; BAB79628.1;
DR EMBL; AB048416; BAB62713.1; JOINED.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Please_Hdc.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 685 AA; 78067 MW; 505E8748E9A6C21F CRC64;

Query Match 90.5%; Score 882; DB 11; Length 685;
Best Local Similarity 90.7%; Pred. No. 2.8e-66;
Matches 176; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MLKQARRPLFRNVLSATQWKVKITRLVQISGASLAEKQKHQDFLIQRTKTKDRRND 60
DB 1 MLKQARRPLFRNVLSATQWKVSTFGQISGAFLERLDKQDFLTRMOTTKDRRND 60
QY 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAI 120
DB 61 EIDKLTGYTKSLLCMPIRNSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAI 120
QY 121 SNAQLFAASRKEYERSALLEVNDLFEEQTDLEKIVKIMHRAQTLKRCRCSVLLED 180
DB 121 SNAQLFAASRKEYERSALLEVNDLFEEQTDLEKIVKIMHRAQTLKRCRCSVLLED 180
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QY 181 IESPVVKFTKSFEL 194
DB 181 IESPVVKFTKSFEL 194

RESULT 3
Q96S76 PRELIMINARY; PRT; 988 AA.
ID Q96S76
AC Q96S76;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=20570133; PubMed=11121118;
RA Yuasa K., Kanoh Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase pDE11A gene:
Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB048423; BAB62713.1;
DR EMBL; AB048402; BAB62713.1; JOINED.
DR EMBL; AB048403; BAB62713.1; JOINED.
DR EMBL; AB048404; BAB62713.1; JOINED.
DR EMBL; AB048405; BAB62713.1; JOINED.
DR EMBL; AB048406; BAB62713.1; JOINED.
DR EMBL; AB048408; BAB62713.1; JOINED.
DR EMBL; AB048409; BAB62713.1; JOINED.
DR EMBL; AB048410; BAB62713.1; JOINED.
DR EMBL; AB048411; BAB62713.1; JOINED.
DR EMBL; AB048412; BAB62713.1; JOINED.
DR EMBL; AB048413; BAB62713.1; JOINED.
DR EMBL; AB048414; BAB62713.1; JOINED.
DR EMBL; AB048415; BAB62713.1; JOINED.
DR EMBL; AB048416; BAB62713.1; JOINED.
DR EMBL; AB048417; BAB62713.1; JOINED.
DR EMBL; AB048418; BAB62713.1; JOINED.
DR EMBL; AB048419; BAB62713.1; JOINED.
DR EMBL; AB048420; BAB62713.1; JOINED.
DR EMBL; AB048421; BAB62713.1; JOINED.
DR EMBL; AB048422; BAB62713.1; JOINED.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 988 AA; 111170 MW; 7F678869353DF7EB CRC64;

Query Match 83.4%; Score 813; DB 4; Length 988;
Best Local Similarity 39.0%; Pred. No. 2.9e-60;
Matches 194; Conservative 0; Mismatches 0; Indels 304; Gaps 1;

QY 1 MLKQARRPLFRNVLSATQWKVKITRLVQISGASLAEKQKHQDFLIQRTKTK----- 54
DB 1 MLKQARRPLFRNVLSATQWKVKITRLVQISGASLAEKQKHQDFLIQRTKTKMAASRL 60
QY 55 ----- 54
DB 61 DFGVETFLDRHPELFDYLMRKQEWKVLQRHSQOGALGPRPSLAGTSSLAHSTC 120
QY 55 ----- 54
DB 121 RGGSSVGGGTGPNGSAHSOPLPGGDCGVPSPSWAGSGRGDGNLQRRASOKELRKSPA 180
QY 55 ----- 54
DB 181 RSKATHVNTYDEQVTSRAQEPPLSSVRRRALLRKASSLPPTTAHLSALLSRSVNLPOYP 240
QY 55 ----- 54
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Db 241 PTAIDYKCHLKKHNEROFFLELVKDISNDLDTLSYSKILIFVCLMVADRCSLFVEGA 300
Qy 55 -----DR 56
Db 301 AAGKTLVSKFFDVHAGTLPPLPCSSSTENSNEVQPGCKGIIGYVGEHGETVNIPIDAYQDR 360
Qy 57 RFNDEIDKLTGYKTKSLCMLPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYLPFC 116
Db 361 RFNDEIDKLTGYKTKSLCMLPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYLPFC 420
Qy 117 GIAISNAQLFAASRKEYERSRALLEVNDLFEETDLEKIYKIMHRAQTLLKCRC 176
Db 421 GIAISNAQLFAASRKEYERSRALLEVNDLFEETDLEKIYKIMHRAQTLLKCRC 480
Qy 177 LLEDIESPVVKFTKSFEL 194
Db 481 LLEDIESPVVKFTKSFEL 498

RESULT 4
Q9HCR9
ID Q9HCR9 PRELIMINARY; PRT; 934 AA.
AC Q9HCR9;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A (Phosphodiesterase 11A4).
GN HSPDE11A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=20469516; PubMed=10906126;
RA Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
RT "Isolation and Characterization of Two Novel Phosphodiesterase PDE11A
RT Variants Showing Unique Structure and Tissue-specific Expression.";
RL J. Biol. Chem. 275:31469-31479(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570133; PubMed=1121118;
RA Yuasa K., Kanoh Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase PDE11A gene:
RT Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB036704; BAB16371.1; -.
DR EMBL; AB048423; BAB62712.1; -.
DR EMBL; AB048403; BAB62712.1; JOINED.
DR EMBL; AB048404; BAB62712.1; JOINED.
DR EMBL; AB048405; BAB62712.1; JOINED.
DR EMBL; AB048406; BAB62712.1; JOINED.
DR EMBL; AB048408; BAB62712.1; JOINED.
DR EMBL; AB048409; BAB62712.1; JOINED.
DR EMBL; AB048410; BAB62712.1; JOINED.
DR EMBL; AB048411; BAB62712.1; JOINED.
DR EMBL; AB048412; BAB62712.1; JOINED.
DR EMBL; AB048413; BAB62712.1; JOINED.
DR EMBL; AB048414; BAB62712.1; JOINED.
DR EMBL; AB048415; BAB62712.1; JOINED.
DR EMBL; AB048416; BAB62712.1; JOINED.
DR EMBL; AB048417; BAB62712.1; JOINED.
DR EMBL; AB048418; BAB62712.1; JOINED.
DR EMBL; AB048419; BAB62712.1; JOINED.
DR EMBL; AB048420; BAB62712.1; JOINED.
DR EMBL; AB048421; BAB62712.1; JOINED.
DR EMBL; AB048422; BAB62712.1; JOINED.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR Pfam; PF01590; GAF; 2.

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DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDG; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 934 AA; 104810 MW; 994675824259447E CRC64;

Query Match 72.7%; Score 709; DB 4; Length 934;
Best Local Similarity 99.3%; Pred. No. 1.7e-51;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 54 KDRFNDEIDKLTGYKTKSLCMLPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYL 113
Db 304 QDRFNDEIDKLTGYKTKSLCMLPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYL 363
Qy 114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEETDLEKIYKIMHRAQTLLKCRC 173
Db 364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEETDLEKIYKIMHRAQTLLKCRC 423
Qy 174 SVLLEDIESPVVKFTKSFEL 194
Db 424 SVLLEDIESPVVKFTKSFEL 444

RESULT 5
Q9VID6
ID Q9VID6 PRELIMINARY; PRT; 935 AA.
AC Q9VID6;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A4.
GN RNPDE11A4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohguru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
RT (PDE11A): comparison of rat and human PDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL; AB059362; BAB79629.1; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDG; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 935 AA; 104570 MW; E80F1039770F8276 CRC64;

Query Match 72.3%; Score 705; DB 11; Length 935;
Best Local Similarity 97.9%; Pred. No. 3.6e-51;
Matches 138; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 54 KDRFNDEIDKLTGYKTKSLCMLPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYL 113
Db 304 QDRFNDEIDKLTGYKTKSLCMLPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYL 363
Qy 114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEETDLEKIYKIMHRAQTLLKCRC 173
Db 364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEETDLEKIYKIMHRAQTLLKCRC 423
Qy 174 SVLLEDIESPVVKFTKSFEL 194
Db 424 SVLLEDIESPVVKFTKSFEL 444

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RESULT 6
Q8VID8
ID Q8VID8 PRELIMINARY; PRT; 581 AA.
AC Q8VID8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A2.
OS RNPDE11A2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohguru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
RT (PDE11A): comparison of rat and human PDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL: AB059360; BAB79627.1; -
DR InterPro: IPR003018; GAF.
DR InterPro: IPR003607; ME_Pplase_HDC.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF01590; GAF; 1.
DR Pfam: PF00233; PDEase; 1.
DR PRINTS: PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_I.
SQ SEQUENCE 581 AA; 66141 MW; 2CA7C2F5DDB37D00 CRC64;

Query Match 44.4%; Score 433; DB 11; Length 581;
Best Local Similarity 100.0%; Pred. No. 1.9e-28;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 VQMYLPFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTL 167
Db 4 VQMYLPFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTL 63

QY 168 LKCRCSVLLLEDIESPVVKTKSPFL 194
Db 64 LKCRCSVLLLEDIESPVVKTKSPFL 90

RESULT 7
Q9HB46
ID Q9HB46 PRELIMINARY; PRT; 576 AA.
AC Q9HB46;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CAMP/cGMP phosphodiesterase 11A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=TESTIS;
RA Hetman J.M., Robas N., Baxendale R., Fidock M., Phillips S.C.,
RA Soderling S.H., Beavo J.A.;
RT "Cloning and characterization of two splice variants of human
RT phosphodiesterase 11A.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).
DR EMBL; AF281865; AAG32023.1; -
DR InterPro: IPR003018; GAF.
DR InterPro: IPR003607; ME_Pplase_HDC.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF01590; GAF; 1.
DR Pfam: PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
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DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 576 AA; 65766 MW; 3992C4C95A5B0B36 CRC64;

Query Match 44.0%; Score 429; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 4.2e-28;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MQMYLPFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTL 168
Db 1 MQMYLPFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTL 60

QY 169 KCRCRSVLLLEDIESPVVKTKSPFL 194
Db 61 KCRCRSVLLLEDIESPVVKTKSPFL 86

RESULT 8
Q95TW8
ID Q95TW8 PRELIMINARY; PRT; 1018 AA.
AC Q95TW8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE GH27433p.
GN CG8279.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J.E., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.W., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY058470; AAL13699.1; -
DR FlyBase; FBgn0038237; CG8279.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR002073; PDEase.
DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF01590; GAF; 2.
DR Pfam: PF00233; PDEase; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_I.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_I.
SQ SEQUENCE 1018 AA; 114668 MW; 8C758A607855EDD9 CRC64;

Query Match 36.4%; Score 354.5; DB 5; Length 1018;
Best Local Similarity 44.8%; Pred. No. 1.6e-21;
Matches 82; Conservative 23; Mismatches 55; Indels 23; Gaps 3;

QY 28 VOISGASLAEOEKHQDFLIQROTQTKDORRENDEIDKLTGYTKSLLCMPIRSSDGEIIG 87
Db 213 IGIAGVMAQTQKQ-----MINIKAYKDARENCEIDLTGYTKNAILCMPICNYEGDIIG 266

QY 88 VQAQINKIPEGAPFETDEDEKVMQVLPFCGIAISNAQLFAASRKEYERSRALLEVNDLF 147
Db 267 VQAQINKTNGCMFEDEHDFEIRRYLTFCGIGIQNAQLFEMSVOEYRNNILLNARSIF 326

QY 148 EEQTDLEKIVKKIMHRAQTLKCRCSVLLLE-----DIESP-----VVKFTK 190
Db 327 EEQNNLECLVTKIMTEARELLKCRCSVFLVDLDCCEASHLEKITEKPNQPATRAIKSAD 386

QY 191 SFE 193
Db 387 SFE 389
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RESULT 9
Q9VFI9
ID Q9VFI9 PRELIMINARY; PRT; 1232 AA.
AC Q9VFI9;
DT 01-MAR-2000 (TReMBLrel. 13, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CG8279 protein.
GN CG8279.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis J.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy K., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003705; AAF5066.2; -.
DR FlyBase; FBgn0038237; CG8279.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDiESTERASE1.
DR PRINTS; PR00387; PDiESTERASE1.
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DR SMART; SM00471; HDC; 1.
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QY 28 VOISGSLAEKQKHQDFLIQRTKTKDRFRNDEIDKLTGYTKTSLLCLPISRSDGELIG 87
DB 326 IGIAGMVAQTKQ-----MINIKAYKQARENCEIDLTKYKTNAILCMPCINVEGDIIG 379
QY 88 VAQAINKIPEGAPFTEDDEKVMQMYLPFCGTAISNAQLFAASRKYEYRSRALLEVVNDLF 147
DB 380 VAQIINKTNGCMFEDEHVEIFRRLYTFCGIGIQAQLFEMSVQYERRNQLILNARSIF 439
QY 148 EEOTDLEKIVKIMHRAOTLLKCRCSVLLLE-----DIESP-----VVKFTK 190
DB 440 EEQNNECLVTKIMFEARELLKCRCSVFLVDLDCCEASHLEKIITEKPNQATRAIKSAD 499
QY 191 SFE 193
DB 500 SFE 502

RESULT 10
Q9VJ79
ID Q9VJ79 PRELIMINARY; PRT; 1284 AA.
AC Q9VJ79;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CG10231 protein.
GN CG10231.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis J.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy K., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003705; AAF5066.2; -.
DR FlyBase; FBgn0038237; CG8279.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDiESTERASE1.
DR PRINTS; PR00387; PDiESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDASE_I; 1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 1232 AA; 137426 MW; ECF6B9C3A71BAF74 CRC64;

Query Match 36.4%; Score 354.5; DB 5; Length 1232;
Best Local Similarity 44.8%; Pred. No. 2.le-21;

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RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003659; AAF53675.1; -.
DR FlyBase: FBgn0032686; CG10231.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR003607; ME_Pplase_Hdc.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF01590; GAF; 2.
DR Pfam: PF00233; PDEase; 1.
DR PRINTS: PR00387; PDIESTERASE1.
DR SMART: SM00665; GAF; 2.
DR SMART: SM00471; Hdc; 1.
DR PROSITE: PS00126; PDEASE_I; 1.
SQ SEQUENCE 1284 AA; 141726 MW; F6873C90A9553430 CRC64;

Query Match 35.8%; Score 349; DB 5; Length 1284;
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Db KKLVSKLFDVCPRTVTEMEQODEVRVWAGTGIAGHVAESGEPVNIPDAYQDERFNCI 322
Qy 63 DKLGYTKSLLCMPIRSSDGEIIGVQAQINKIPEGAPFTTDEDEKVMQMLPFCGIAISN 122
Db DLSLTGYRTKALLCPIKDSGSDVIGVAQVINKM-NGECFSIDEKVFSSYLQFCGIGLRN 381
Qy 123 AOLFAASRKEYERSRALLEVVNDLFEETDLEKIVKIMHRAQTLKLCERCSCVLLLEDIE 182
Db AOLKEKSLKRNQVLDLARMIFEOSTIEHVMVFRILTHMQSLIOCORVOILLVHEAD 441
Qy 183 SPVVKFTKSFE 193
Db 442 KG--SFSRVFD 450

RESULT 11
ID Q9GQU6 PRELIMINARY; PRT; 930 AA.
AC Q9GQU6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cyclic nucleotide phosphodiesterase.
GN PDE.
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RA Rascon A., Soderling S.H., Beavo J.A.;
RT "Cloning and characterization of a cyclic nucleotide phosphodiesterase
from Trypanosoma brucei."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF192755; AAG43461.1; -.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR003607; ME_Pplase_Hdc.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF01590; GAF; 2.
DR Pfam: PF00233; PDEase; 1.
DR PRINTS: PR00387; PDIESTERASE1.
DR SMART: SM00665; GAF; 2.
DR SMART: SM00471; Hdc; 1.
DR PROSITE: PS00126; PDEASE_I; 1.
SQ SEQUENCE 930 AA; 103269 MW; 4E297F6347F59A29 CRC64;

Query Match 20.8%; Score 203; DB 5; Length 930;
Best Local Similarity 35.3%; Pred. No. 9.3e-09;
Matches 48; Conservative 31; Mismatches 43; Indels 14; Gaps 4;

Qy 55 DRRENDEIDKLTGYTKSLLCMPIRSSDGEIIGVQAQINKIPEGAPFTTDEDEKVMQMLPFCGIAISN 104
Db 302 DDRFNREVDKATGYRTKILCPV-MYEGTIVAVAQILNKLDLTSTESGLRLPR--VFGKR 358

Qy 105 DEKVMQMLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEETDLEKIVKIMHRAQTLKLCER 163
Db DEELFQTFSEFAGASLRNCRINDRLLEKKKSDVILDVVTLSNTDTRDVGIVPHALHG 418
Qy 164 AOTLLKERCSCVLLLE 179
Db AKLLNADRSTFLVLD 434

RESULT 12
ID Q8R0D4 PRELIMINARY; PRT; 836 AA.
AC Q8R0D4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to phosphodiesterase 6C, CGMP specific, cone, alpha
prime.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC027050; AAH27050.1; -.
SQ SEQUENCE 836 AA; 95906 MW; A8D60FAAFE6C9D9E CRC64;

Query Match 20.6%; Score 201; DB 11; Length 836;
Best Local Similarity 37.8%; Pred. No. 1.2e-08;
Matches 48; Conservative 26; Mismatches 49; Indels 4; Gaps 3;

Qy 54 KDRFNDEIDKLTGYTKSLLCMPIRSSDGEIIGVQAQINKIPEGAPFTTDEDEKVMQMLPFCGIAISN 112
Db KNSHFSDFMDKOTGYVTRNLLAVIVAGK-EVLAVVMVAVNKI--SAPEFSKQDEEVFSKY 216
Qy 113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEETDLEKIVKIMHRAQTLKLCER 172
Db LSFVAVALRLQHTSYLSVESRRSQILMWSANKVFEELTDVERQFHKALYTIRTYLNCNR 276
Qy 173 CSVLLLE 179
Db 277 YSIGLLD 283

RESULT 13
ID Q91ZQ1 PRELIMINARY; PRT; 861 AA.
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE cGMP phosphodiesterase 6c.
GN PDE6C
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=RETINA;
RA Chang B., Hawes N.L., Hurd R.E., Davisson M.T., Nusinowitz S.,
RA Heckenlively J.R.;
RT "A sequence alteration in Pde6c gene causes cone photoreceptor
function loss (cpfl1) in mice."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF411063; AAK96254.1; -.
DR MGD: MGI:105956; Pde6c.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR002073; PDEase.
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 10:43:55 ; Search time 5414 Seconds
(without alignments)
11170.231 Million cell updates/sec

Title: US-09-663-542-2

Perfect score: 2078

Sequence: 1 ggccgagatgctgaagcag.....actaataactcgaggcatgc 2078

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_btg.*

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4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

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10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rnd.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2078	100.0	2078	6	AX139462	AX139462 Sequence
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3	2056.4	99.0	3507	9	AB038041	AB038041 Homo sapi
4	1891.8	91.0	4476	9	AB036704	AB036704 Homo sapi
5	1734.8	83.5	2141	9	AF281865	AF281865 Homo sapi
6	1684	81.0	3492	10	AB059361	AB059361 Rattus no
7	1551.4	74.7	4170	10	AB059362	AB059362 Rattus no
8	1503.8	72.4	1784	9	HSA251509	AJ251509 Homo sapi
9	1414.4	68.1	3098	10	AB059360	AB059360 Rattus no
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11	417.8	20.1	5687	3	AX122262	AY122262 Drosophill
12	388.8	18.7	426	6	AX375673	AX375673 Sequence
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14	356.6	17.2	2499	6	E52149	E52149 Novel prote
15	356.6	17.2	2645	6	AX036123	AX036123 Sequence
16	356.6	17.2	2645	6	I58538	I58538 Sequence 22
17	356.6	17.2	2645	6	I87013	I87013 Sequence 22
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19	356.6	17.2	4415	9	D89094	D89094 Homo sapien
20	355	17.1	2172	6	E52146	E52146 Novel prote
21	355	17.1	2499	6	E52145	E52145 Novel prote
22	355	17.1	2540	9	AB015656	AB015656 Homo sapi
23	355	17.1	3041	9	HSPDE5A1	AJ004865 Homo sapi
24	355	17.1	3381	6	AX024038	AX024038 Sequence
25	353.4	17.0	2908	4	AB008467	AB008467 Canis fam
26	353.4	17.0	4232	4	AB008468	AB008468 Canis fam
27	352.6	17.0	4857	3	AY058470	AY058470 Drosophill
28	345.2	16.6	1982	6	AX036113	AX036113 Sequence
29	345.2	16.6	1982	6	I58528	I58528 Sequence 12
30	345.2	16.6	1982	6	I87003	I87003 Sequence 12
31	343.6	16.5	2913	4	BTPDE5A1A	L16545 Bovine cGMP
32	343.6	16.5	4474	6	I58526	I58526 Sequence 9
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36	231	11.1	2724	10	BC029810	BC029810 Mus muscu
37	226.2	10.9	3980	10	RNU21101	U21101 Rattus norv
38	219.2	10.5	2406	6	E60014	E60014 Novel phosp
39	219.2	10.5	2412	9	AB026816	AB026816 Homo sapi
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45	217.6	10.5	3195	6	AR116119	AR116119 Sequence

ALIGNMENTS

RESULT 1
AX139462

LOCUS

DEFINITION

AX139462

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

REFERENCE

AUTHORS

TITLE

JOURNAL

AX139462 Sequence 2 from Patent EP1085089.
AX139462
AX139462.1 GI:14275107

2078 bp
DNA

linear PAT 30-MAY-2001

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2078)
Fidock,M.D. and Kobas,N.M.
Human cyclic nucleotide phosphodiesterase
Patent: EP 1085089-A 2 21-MAR-2001;

Pfizer Limited (GB) ; PFIZER INC. (US)			
FEATURES	Location/Qualifiers		
	Source		
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/db_xref="taxon:9606"			
BASE COUNT	615 a 439 c 491 g 533 t		
ORIGIN			
Query Match	100.0%; Score 2078; DB 6; Length 2078;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 2078;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	1	GGTCCGAGATGCTGAAGCAGGCAAGAGACCTTTATTTCAGAAATGTGCTCAGTGCCACAC	60
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Db	61	AGTGGAAAAGGTGAATATCACAGACTGGTCCAAATCTCTGGGGCCCTCTTTGGCTGAAA	120
QY	121	AACAGGAAAAGCACCAGGATTTCTTATACAGAGGCAACAAACAAACAAAGGATCGACGAT	180
Db	121	AACAGGAAAAGCACCAGGATTTCTTATACAGAGGCAACAAACAAACAAAGGATCGACGAT	180
QY	181	TCAATGATGAATCGACAAGCTGACTGGATACAGACAAATATTTATTTGTCATGCCCTA	240
Db	181	TCAATGATGAATCGACAAGCTGACTGGATACAGACAAATATTTATTTGTCATGCCCTA	240
QY	241	TCCGAAGCAGTGATGGTGAGATTAATTTGGTGGCCCCAAGCGATAAATAAGATTCCTGAAG	300
Db	241	TCCGAAGCAGTGATGGTGAGATTAATTTGGTGGCCCCAAGCGATAAATAAGATTCCTGAAG	300
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Db	301	GAGCTCCATTTACTGAAGATGATGAAAAGTTATGCGAGATGTATCTTCCATTTTGTGGAA	360
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Db	361	TCGCCATATCTAAGCTCAGCTCTTTGCTGCTCAAGGAAGAAATATGAAAGAGCAGAG	420
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Db	421	CTTTGCTAGAGTGTTAATGACCTCTTTTGAAGAACAGACTGACCTGGAGAAAATTTGTCA	480
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Db	721	TCAGTGTGCTTACCAGGATCCGGCTTTGATGAGAGGAGCAGATATCTGGTTTTTC	780
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Db	781	ACATAAGATCTGTTCTTTGTGCTCCTATTTTGGAAATAGCAACCAACCAATTAATTTGGAGTGG	840
QY	841	CTCAAGTGTAAACAGACTTGTGGGAAACCTTTTGGATGATGAGATCAACGACTTTTTC	900
Db	841	CTCAAGTGTAAACAGACTTGTGGGAAACCTTTTGGATGATGAGATCAACGACTTTTTC	900
QY	901	AGGCTTTTGTATCTTTTGTGGACTTGGCATCAACAACAATTAATGATGATCAAGTGA	960
Db	901	AGGCTTTTGTATCTTTTGTGGACTTGGCATCAACAACAATTAATGATGATCAAGTGA	960
QY	961	AGAACTCTCGGGCAAGCAGTCTGTGGCTCTTGTGATGTGCTATCATACCAACATGTT	1020
Db	961	AGAACTCTCGGGCAAGCAGTCTGTGGCTCTTGTGATGTGCTATCATACCAACATGTT	1020
QY	1021	CAAAAGCTGAAGTTGACAAGTTTAAAGCAGCAACATCCCTCTGGTGTGCAGAACTTGCCA	1080
Db	1021	CAAAAGCTGAAGTTGACAAGTTTAAAGCAGCAACATCCCTCTGGTGTGCAGAACTTGCCA	1080
QY	1081	TCGATGACATTCATTTTTCATGACTTTTCTCTCGACGTTGATGCCATGATCAGACTGCTC	1140
Db	1081	TCGATGACATTCATTTTTCATGACTTTTCTCTCGACGTTGATGCCATGATCAGACTGCTC	1140
QY	1141	TCCGGATGTTTCATGGAGCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGT	1200
Db	1141	TCCGGATGTTTCATGGAGCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGT	1200
QY	1201	GTAGGTGCTTTTTCACAGTGAGGAAAACTATCGGATGGTTCTTATACCACAACTGGAGAC	1260
Db	1201	GTAGGTGCTTTTTCACAGTGAGGAAAACTATCGGATGGTTCTTATACCACAACTGGAGAC	1260
QY	1261	ATGCCCTTCAACGCTGTGTGAGCTGATGTTTCGCGATGTTTAAACCACTGCTGGGTTTCAAGACA	1320
Db	1261	ATGCCCTTCAACGCTGTGTGAGCTGATGTTTCGCGATGTTTAAACCACTGCTGGGTTTCAAGACA	1320
QY	1321	TTCTGACCCAGGTGGAAATTTTACCGGTGATTTGFGGATGCTGTCATGACCTCGACC	1380
Db	1321	TTCTGACCCAGGTGGAAATTTTACCGGTGATTTGFGGATGCTGTCATGACCTCGACC	1380
QY	1381	ACAGGGGAAACCAAACTGCTTCCAAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATG	1440
Db	1381	ACAGGGGAAACCAAACTGCTTCCAAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATG	1440
QY	1441	GAACCTCTGCTTACCTTGGAGCATCACCATTTCACACCGCGGTGATGATCTTCAAAGTG	1500
Db	1441	GAACCTCTGCTTACCTTGGAGCATCACCATTTCACACCGCGGTGATGATCTTCAAAGTG	1500
QY	1501	AGGTGCACAATATCTTTGCTTAACTGCTTCCCAAGGAATATAGTGACCTTATGACGCTTT	1560
Db	1501	AGGTGCACAATATCTTTGCTTAACTGCTTCCCAAGGAATATAGTGACCTTATGACGCTTT	1560
QY	1561	TGAAGCAGTCAATATTTGGCAACAGACCTCAGCTGTTACTTTTGAAGAGAGAACTCAATTC	1620
Db	1561	TGAAGCAGTCAATATTTGGCAACAGACCTCAGCTGTTACTTTTGAAGAGAGAACTCAATTC	1620
QY	1621	TTGAACCTTGTGCTTAAAGGAGAAATGCGATTGGAACATCAAAAACCATCTGATATATTC	1680
Db	1621	TTGAACCTTGTGCTTAAAGGAGAAATGCGATTGGAACATCAAAAACCATCTGATATATTC	1680
QY	1681	GATCAATGTTAATGACAGCTGTGACCTTGGAGCCGTGACCAACCGTGGGAGATCTCCA	1740
Db	1681	GATCAATGTTAATGACAGCTGTGACCTTGGAGCCGTGACCAACCGTGGGAGATCTCCA	1740
QY	1741	GACAGGTGGCAGAACTTTGTAACCACTGAGTTCTTCGAAACAGGAGATCGGGAGAGATTAG	1800
Db	1741	GACAGGTGGCAGAACTTTGTAACCACTGAGTTCTTCGAAACAGGAGATCGGGAGAGATTAG	1800
QY	1801	AGCTCAAACTCCTCTTTCAGCAATTTTTCGAAACCGGAGGATGAACCTGCTCGGT	1860
Db	1801	AGCTCAAACTCCTCTTTCAGCAATTTTTCGAAACCGGAGGATGAACCTGCTCGGT	1860
QY	1861	TGCAACTGGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1920
Db	1861	TGCAACTGGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1920
QY	1921	ACGTGAAACTGAAGCCGATGCTAGATTAGTACAAACAGAAAGTAAAGTGGCAAGAGC	1980
Db	1921	ACGTGAAACTGAAGCCGATGCTAGATTAGTACAAACAGAAAGTAAAGTGGCAAGAGC	1980
QY	1981	TACACCAAAACGACTGCTGGCCCTCAACTGCTTCCCTCCTCCTCCTCCTCCTCCTCCT	2040
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Db	1981.	TACACCAAAAGAGCTGCTGGCCTCAACTGCTCTACCTCTCTCCCTGCCAGTGTATGCG	2040
Qy	2041	TAGCCAAGGAGACAGGAACTAATAACTCGAGGATGC	2078
Db	2041	TAGCCAAGGAGACAGGAACTAATAACTCGAGGATGC	2078
RESULT 2			
HSA278682			
LOCUS			
DEFINITION		HSA278682 2502 bp mRNA linear PRI 09-NOV-2000	
ACCESSION		11A3 (PDE11A3 gene).	
VERSION		AJ278682	
KEYWORDS		CAMP/CGMP cyclic nucleotide phosphodiesterase 11A3; PDE11A3 gene.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 2502)	
JOURNAL		Hetman,J.M., Robas,N., Baxendale,R., Fidock,M., Phillips,S.C.,	
MEDLINE		Soderling,S.H. and Beavo,J.A.	
PUBMED		Cloning and characterization of two splice variants of human	
REFERENCE		phosphodiesterase 11A	
AUTHORS		Proc. Natl. Acad. Sci. U.S.A. 97 (23), 12891-12895 (2000)	
TITLE		1. 2502	
JOURNAL		Location/Qualifiers	
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AUTHORS		FLIQROTTKDRRDEIDKLTGYKTSLLCMPISRSDEIGIYVAQAINKIPEGAPFT	
TITLE		EDDEKVMQYLPFCGIATISNAQLFAASRKEYERSRALLEVNDLFEOTDLEKIVKKI	
JOURNAL		MIRAQTLKLCERCSVLLLEDIESPVVKETKSELMSPKCSADAENSPRESMEKSSYSD	
MEDLINE		WLNNISALVASTGLPWNISDAVDQPRDAEDQISGFHRSVLCVPIWNSHRIIG	
PUBMED		VAQUNRUDGPFDDQRLFEAFVIFCGLGINNITMYDQVKKSVKQSVLVDLSHY	
REFERENCE		ATCSKAEDYKKAANIPLVSELAIDDIHDFDLSLDVAMITAAALRMFMELGWQFKFI	
AUTHORS		DYETLCRWLLTVRNRYRMVLYHNWRHAFNVCLMAMTAGFODILFEVELAVIVG	
TITLE		CLCHDLHRGTNNAFOAKSGSALAOLYGTSALEHHHFNHVMILQSEGHNFANLSS	
JOURNAL		KEYSDLMOLLKQSLATDLTYLFFERTEFFELVSKGEYDWNIKHRDIFRSMWTACD	
MEDLINE		LGAVTKPWEISQVAELVTSFEFFQDGRERLEKLTPTSAIFDRNRKDELPLQLEWDI	
PUBMED		SICMPLYQALVKNVKKLPMLDVSATNRSKWEELHQKRLLASTASSSSPASVMVAKED	
REFERENCE		RN"	
BASE COUNT		731 a 544 c 618 g 606 t 3 others	
ORIGIN			
Query Match		/ 99.0%; Score 2058; DB 9; Length 2502;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 2058; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
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Db 397 CATTACTGAAGATGATGAAGAAAGTTATGACAGATGATCTTCCATTTTGTGGAATGCGC 456
QY 366 ATATCTAAGCCTCAGCTCTTTGCTGCCTCAAGGAAAGAAATATGAAGAGCAGAGCTTTG 425
Db 457 ATATCTAAGCCTCAGCTCTTTGCTGCCTCAAGGAAAGAAATATGAAGAGCAGAGCTTTG 516
QY 426 CTAGAGGTGGTTAATGACCTCTTTGAAGACAGATGACCTGGAGAAATTTGCAAGAA 485
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Db 577 ATAATGCATCGGCGCCAAACTCTGCTGAATGATGAGCGCTGTCGTTTACTCTAGAG 636
QY 546 GACATCGAATCACCACTGAGTGGTGAATTTACCAATCTTTGAATGATGTCGCCAAAGTGC 605
Db 637 GACATCGAATCACCACTGAGTGGTGAATTTACCAATCTTTGAATGATGTCGCCAAAGTGC 696
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Db 757 CTAATAAATAACAGCATGCTGAGCTGTTGCTTCAACAGGCTTCCAGTGAACATCACT 816
QY 726 GATGCTACCAAGATCCGCGCTTTGATGACAGAGCAGACCATATCTGTTTTCACATA 785
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QY 1266 TTCAACGCTGTGTCAGCTGATGTTCCGCGATGTTAAGCACTGCTGGGTTTCAAGACATTCG 1325
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QY 1326 ACCGAGGTGGAAATTTTACGCGTGATGTTGGGATGCCTGTGTCATGACCTCGACACACAGG 1385
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Db 1477 GGAACCAACAATGCCTTCCAAAGCTAAGATGGCTCTGCCCTGGCCCAACTCTATGGAACC 1536
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Db 1537 TCTGCTACCTTGGAGCATCACCATTTCAACACCGCGTGATGATCTTCAAAAGTGAAGGT 1596
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Db 1717 CTTGTCAGTAAAGGAGAAATACGATTGGAACATCAAAAACCATCGTATATATTTCCATCA 1776
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QY 1806 AAACCTCACTCTCTCAACCAATTTTTCGGAACCGGAGGATCAACTGCTCGTTTGCAA 1865
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QY 1866 CTGGAGTGGATGATAGCATCTGCACTGCTTTGATGATGAGGACTGCTGAAGGTCAACGTG 1925
Db 1957 CTGGAGTGGATGATAGCATCTGCACTGCTTTGATGATGAGGACTGCTGAAGGTCAACGTG 2016
QY 1926 AAACCTCAACCCCATCTAGATTCAGTACAAACAGAGTAAGTGGGAGAGCTACAC 1985
Db 2017 AAACCTCAACCCCATCTAGATTCAGTACAAACAGAGTAAGTGGGAGAGCTACAC 2076
QY 1986 CAAAACGACTGCTGGCTTCAACTGCTCATCTCTCCCTGCCAGTGTATGTTAGGCC 2045
Db 2077 CAAAACGACTGCTGGCTTCAACTGCTCATCTCTCCCTGCCAGTGTATGTTAGGCC 2136
QY 2046 AAGGAAGACAGGAATAA 2063
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RESULT 4
AB036704
LOCUS
DEFINITION Homo sapiens HSPDE11A mRNA for phosphodiesterase 11A, complete cds.
ACCESSION AB036704
VERSION AB036704.1 GI:10716051
KEYWORDS phosphodiesterase 11A.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Yuasa,K., Kotera,J., Fujishige,K., Michibata,H., Sasaki,T. and Omori,K.
TITLE Isolation and characterization of two novel phosphodiesterase PDE11A variants showing unique structure and tissue-specific expression
JOURNAL J. Biol. Chem. 275 (40), 31469-31479 (2000)
MEDLINE 20469516
REFERENCE 2 (bases 1 to 4476)
AUTHORS Omori,K. and Yuasa,K.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-2000) Kenji Omori, Tanabe Seiyaku Co. Ltd., Discovery Research Laboratory; 2-50 Kawagishi-2-chome, Toda, Saitama 335-8505, Japan (E-mail:k-omori@tanabe.co.jp, Tel:+81-48-433-8069, Fax:+81-48-433-8159)

FEATURES	Location/Qualifiers	Query	1769	TTCCAGTGAACATCACTGATGCTTACAGGATCCGCGCTTTGATGCAGAGCAGACCAGA	768
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	VNDLFEOTDLEKIVKIMHRAQTLLKERCSSLLELDESVPVKTSPFELMSPKCS	Ds	2189	TCACAGCTGCTCTCCGGATGTTTCATGGAGCTGGGATGGTACAGAAATTTAAATTTGACT	2248
	ADAERSFRESMEKSSYSDWLNNSTIAELVASTGLPVLNDSATQDPRFAEADQISGFH	QY	1189	ATGAGACACTGTGTAGTGGCTTTTTCACAGTGAAGAAACATTCGGATGTTTCTATACC	1248
	IKSVLCVPLWNSHQILGVAQVNLNRDGPFPDDADORLFEAFVIFCGLGINNTIMYDQ	Ds	2249	ATGAGACACTGTGTAGTGGCTTTTTCACAGTGAAGAAACATTCGGATGTTTCTATACC	2308
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	ASTASSSPASVMAKEDRN"	QY	1429	CCCAACTCTATGGAACCTCTGCTACCTTTGGAGCATCACCATTTCAACACGCGGTGATGA	1488
BASE COUNT	1260 a 980 c 1109 g 1127 t	Ds	2489	CCCAACTCTATGGAACCTCTGCTACCTTTGGAGCATCACCATTTCAACACGCGGTGATGA	2548
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QY	229 TGTGATGCTTATCGAAGCACTGATGAGATTTATGGTGTGGCCCAAGCGATAATA	QY	1669	GTGATATATTTGATCAATGTTTAAAGAGCTGTGACCTTTGGAGCCGTGACCAACCGT	1728
Ds	1289 TGTGATGCTTATCGAAGCACTGATGAGATTTATGGTGTGGCCCAAGCGATAATA	Ds	2729	GTGATATATTTGATCAATGTTTAAAGAGCTGTGACCTTTGGAGCCGTGACCAACCGT	2788
QY	289 AGATTCCTGAAGAGCTCCATTTACTGAAGATGATGAAAGCTTATGAGATGATCTTC	QY	1729	GGGAGATCTCCAGACAGCTGGCAGAACTTTGTAACAGTGTGTTCTTCAACAGAGATC	1788
Ds	1349 AGATTCCTGAAGAGCTCCATTTACTGAAGATGATGAAAGCTTATGAGATGATCTTC	Ds	2789	GGGAGATCTCCAGACAGCTGGCAGAACTTTGTAACAGTGTGTTCTTCAACAGAGATC	2848
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Ds	1409 CATTTTGTGGAATGCCATATCTAAGCTCAGCTCTTTGCTGCCCTCAAGGAAAGATATG	Ds			
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QY	649 CATCATCTCCGACTGGCTTAATAAATACAGCATTTGCTGAGCTGGTCTTCAACAGGCC	QY			
Ds	1709 CATCATCTCCGACTGGCTTAATAAATACAGCATTTGCTGAGCTGGTCTTCAACAGGCC	Ds			

Db	2849	GGAGAGATTAGAGCTCAAACTCACTCTCTCAGCAATTTTGGATCGGAACCGGAAGGATG	2908	
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Db	2909	AACTGCCTCGGTGCAACTGGAGTGGATTGATAGCATCTGCATGCCCTTTGTTATCAGGCAC	2968	
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Db	2969	TGTTGAGGTCAACCTGAACTGAAGCGATGCTAGATTGATGAGTACAAACAGAAGTA	3028	
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LOCUS	AF281865	2141 bp	linear	PRI 14-NOV-2000
DEFINITION	Homo sapiens cAMP/cGMP phosphodiesterase 11A2 mRNA, complete cds, alternatively spliced.			
ACCESSION	AF281865			
VERSION	AF281865.1	GI:11141610		
KEYWORDS				
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Hetman,J.M., Robas,N., Baxendale,R., Fidock,M., Phillips,S.C., Soderling,S.H. and Beavo,J.A.			
TITLE	Cloning and characterization of two splice variants of human phosphodiesterase 11A			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (23), 12891-12895 (2000)			
MEDLINE	20524097			
PUBMED	11050148			
REFERENCE	2 (bases 1 to 2141)			
AUTHORS	Hetman,J.M., Soderling,S.H. and Beavo,J.A.			
TITLE	Direct Submission			
JOURNAL	Submitted (23-JUN-2000) Pharmacology, University of Washington, 1959 NE Pacific St., Seattle, WA 98195, USA			
FEATURES	Location/Qualifiers			
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Best Local Similarity	99.9%;	Pred. No. 0;		

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RESULT 7

LOCUS AB059362 4170 bp mRNA linear ROD 18-JAN-2002
DEFINITION Rattus norvegicus RNPDE11A4 mRNA for phosphodiesterase 11A4,
complete cds.
ACCESSION AB059362
VERSION AB059362.1 GI:18143352
KEYWORDS Rattus norvegicus cDNA to mRNA.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
Yusua, K., Ohgaru, T., Asahina, M. and Omori, K.
Identification of rat cyclic nucleotide phosphodiesterase 11A
(PDE11A): comparison of rat and human PDE11A splicing variants
Eur. J. Biochem. 268 (16), 4440-4448 (2001)
21393948
2 (bases 1 to 4170)
Yusua, K. and Omori, K.
Direct Submission
Submitted (04-APR-2001) Kenji Omori, Tanabe Seiyaku Co. Ltd.,
Discovery Research Laboratory; 2-2-50 Kawagishi, Toda, Saitama
335-8505, Japan (E-mail:k-omori@tanabe.co.jp, Tel:81-48-433-8068,
Fax:81-48-433-8159)
LOCATION/Qualifiers
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BASE COUNT 1100 a 1004 c 1067 g 999 t
ORIGIN

Query Match 74.7%; Score 1551.4; DB 10; Length 4170;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 216; Indels 3; Gaps 1;

QY	169	AGGATCGAGGATCAATGATGAATCGACAGCTGACTGGATACAGACAAAATCATTTAT	228
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QY	229	TGTGATGCTATCCGAAGCAGTGTGATGAGATTATTTGGTGTGGCCCAAGCGATAAATA	288
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QY	289	AGATTCTCGAAGAGCTCCATTACTGAAGATGATGAAGAAAGTTATGAGAGTATCTTC	348
DB	1199	AGGTTCTCGAGGGTGTCTCCATTACAGAAAGACGACGAAAGAAAGTTATGAGATGTATCTTC	1258
QY	349	CATTTTGTGGATCCCATATCTACGCTCAGCTCTTTGCTGCTCAAGGAAGAAATG	408
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QY	409	AAAGAGCAGAGCTTTGTAGAGTGGTTAATGACCTCTTTGAAGAACAGACTGACCTGG	468
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QY	469	AGAAATTTGCAAGAAATATATGATCGGGCCCAACCTCTGCTGAAATGTGAGCGCTGT	528
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QY	529	CTGTTTTACTCTACAGGACATCGAATCACCAGTGGTGAATTTTACCATACTTTTGAAT	588
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QY	589	TGATGTCCTCCAAAGTGCAGTGTGATGCTGAGAAGCAGTTTCAAGAAAGCAGTGAAGAT	648
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QY	949	ATGATCAAGTGAAGAGCTCTGGGCAAGCAGCTGTGGCTTTGATGTGATCATATACC	1008
DB	1859	ATGACCAAGTGAAGAGCTCTGGGCAAGCAGCTGTGGCTTTGATGTGATGATGATGATGAT	1918
QY	1009	ATGCAACATGTTCAAGCTGAGTTGACAGTTTAAAGCGACCCAAACATCCCTCTGGTGT	1068

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HSA251509

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QY	1369	ATGACCTCGACACAGGGGAACCAACATGCTTCCAAAGCTAAGAGTGGCTTGCCTGG	1428
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QY	1489	TCCTTCAAGTGAAGGTCACAAATATCTTGTGCTTCCCTTCCAAAGAAATATAGTACC	1548
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QY	1549	TTATGACAGCTTTTGAAGCAGTCAATATTTGGCAACAGACCTCACGCTGTACTTTGAGAGA	1608
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QY	1609	GAATGAAATCTTGAACCTTGTCAAGTAAAGAGATACGATTGGAACATCAAAACCATC	1668
DB	2519	GAATGAAATCTTGAACCTTGTCAAGTAAAGAGATACGATTGGAACATCAAAACCATC	2578
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DB	2879	AGTGGGAAGACTACACCAAAACGACTGCTGGCTCAACTGCCTTTCCTCTCTCC	2938
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LOCUS	HS25151509	1784 bp	mRNA	linear	PRI 23-MAR-2000
DEFINITION	Homo sapiens mRNA for cyclic nucleotide phosphodiesterase 11A1 (PDE11A gene).				
ACCESSION	AJ251509				
VERSION	AJ251509.1	GI:7327960			
KEYWORDS	cyclic nucleotide phosphodiesterase 11A1; PDE11A gene.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1784)				
AUTHORS	Fawcett,L., Baxendale,R., Stacey,P., McGrouther,C., Harrow,I., Soderling,S., Hetman,J., Beavo,J.A. and Phillips,S.C.				
TITLE	Molecular cloning and characterization of a distinct human phosphodiesterase gene family: PDE11A				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3702-3707 (2000)				
MEDLINE	20202699				
PUBMED	10725373				
REFERENCE	2 (bases 1 to 1784)				
AUTHORS	Phillips,S.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-DEC-1999) Phillips S.C., Discovery Biology, Pfizer Central Research, Ramsgate Road, Sandwich, Kent CT13 9NJ, UNITED KINGDOM				
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QY	617	TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA	676		
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Qy 2057 GAACTAA 2063
Db 1617 GAACTAA 1623

RESULT 9
AB059360
LOCUS AB059360 3098 bp mRNA linear ROD_18-JAN-2002
DEFINITION Rattus norvegicus RNPDE11A2 mRNA for phosphodiesterase 11A2,
complete cds.
ACCESSION AB059360
VERSION AB059360.1 GI:18143348
KEYWORDS Rattus norvegicus cDNA to mRNA.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1
Yusa,K., Ohguru,T., Asahina,M. and Omori,K.
Identification of rat cyclic nucleotide phosphodiesterase 11A
(PDE11A): comparison of rat and human PDE11A splicing variants
Eur. J. Biochem. 268 (16), 4440-4448 (2001)
2 (bases 1 to 3098)
Yusa,K. and Omori,K.
Direct Submission
Submitted (04-APR-2001) Kenji Omori, Tanabe Seliyaku Co. Ltd.,
Discovery Research Laboratory, 2-2-50 Kawagishi, Toda, Saitama
335-8505, Japan (E-mail:k-omori@tanabe.co.jp, Tel.81-48-433-8068,
Fax:81-48-433-8159)

FEATURES

Location/Qualifiers
1..3098
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BASE COUNT
ORIGIN

Query Match 68.1%; Score 1414.4; DB 10; Length 3098;

Best Local Similarity 88.4%; Pred. No. 0;
Matches 1548; Conservative 0; Mismatches 201; Indels 3; Gaps 1;
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QY 2067 CTCGAGGATGC 2078
Db 1908 ACCAGAGCTGC 1919

RESULT 10
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LOCUS
DEFINITION Homo sapiens cDNA FLJ23693 fis, clone HEP10314, highly similar to
Homo sapiens mRNA for cyclic nucleotide phosphodiesterase 11A1.
AK074273
ACCESSION
VERSION AK074273.1 GI:18676829
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens; hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
clone:HEP10314.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
TITLE
JOURNAL
REFERENCE
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.

TITLE Direct Submission
JOURNAL Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnalists.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing; Department of Virology and Human
Genome Center, Institute of Medical Science, University of Tokyo
(partly supported by Science and Technology Agency).
FEATURES
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Qy	1909	TGGTGAAGGTCAAGCTGAACTGAAGCGGATGCTAGATTTCAGTAGCTACAAACAAGATA	1968
Db	3919	TTGCCACCTCTCCGACAAGCTTGAGGCTCTTTGTCGAGGGGTGCGGGATAATCGAGGCC	3978
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Db	3979	ATTGGATTGATCT 3991	
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LOCUS	AX375673	426 bp	DNA linear PAT 01-MAR-2002
DEFINITION	Sequence 4 from Patent WO2000854.		
ACCESSION	AX375673		
VERSION	AX375673.1	GI:19170221	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Ramakrishnan,S.		
TITLE	Regulation of human phosphodiesterase-like enzyme		
JOURNAL	Patent: WO 0200854-A 4 03-JAN-2002;		
FEATURES	Bayer Aktiengesellschaft (DE)		
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Qy	411	AGAAGCAGAGCTTTGCTAGAGGTGGTTAATCACCTCTTTGAAGAACACAGCTGACCTGAG	470
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DEFINITION     E52150
ACCESSION      E52150
VERSION        E52150.1 GI:18622238
KEYWORDS       JP 2000354492-A/6.
SOURCE         Homo sapiens.
ORGANISM       Homo sapiens
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               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 2172)
AUTHORS        Tarui,N., Tsuchiya,T. and Nakahama,K.
TITLE          Novel protein and DNA thereof
JOURNAL        Patent: JP 2000354492-A 6 26-DEC-2000;
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COMMENT        OS Homo sapiens (human)
               PN JP 2000354492-A/6
               PD 26-DEC-2000
               PF 19-JUL-1999 JP 1999204336
               PR
               PI NAKOI TARUI,TAKAYUKI TSUCHIYA,KAZUO NAKAHAMA
               PC C12N15/09,C07K16/40,C12N1/21,C12N9/16,C1201/34//A61K38/46, PC
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ORIGIN

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Best Local Similarity 52.0%; Pred. No. 2e-86;
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Db 1125 GTCGTATCATGCTTCAGCAGCAGGAGGAAGAAACAAGAGAGCTTACAGTCTGTAGCGGCTGC 1184
QY 1061 TCTGGTGTCA-----GAACTTGCATCGATGACATTCATTTTGTGATGACTTTCTCT 1111
Db 1185 TGTGTCATCTGCCAGACCCCTTAAATTTACTGACTTTAGCTTTCAGTGTGAGCT 1244
QY 1112 CGAGTGTGATGCCATGATCACAGTGTCTCCGATGTTTCATGAGCTGGGATGGTACA 1171
Db 1245 CTCATCTGGAACACAGCACTGTGTACAAATTCGGATGTTTACTGACCTCAACCTTGTGCA 1304
QY 1172 GAAATTTAAATTTGACTATGAGACACTGTGTAGGTGGCTTTTGGACAGTGAAGAAAAC 1231
Db 1305 GAACTTCCAGATGAACATGAGGTTCTTTGAGATGAGATTTTAAAGTGTAAAGAAATTA 1364
QY 1232 TCGGATG---GTTCTTATACCACAACTGGAGACATGCCCTTCAACGTGTGTGACGTGATGT 1288
Db 1365 TCGGAGAAATGTTGCCCTATCATATTTGAGACATGCCCCTTTAATACAGCTCAGTGTGAT 1424
QY 1289 CGCGATGTTAAACCACTGCTGGGTTTCAAGACATTTCTGACCGAGGTGGAATTTTACGG 1348
Db 1425 TGCTGCTCTAAAGCAGGCAAAATTCAGAACAAGCTGACTGACCTGGAGACTTTGCAT 1484
QY 1349 GATTGTGGATGCCCTGTGTCTGACCTCGACCAAGGGAACCAACATGCCTTCCAAGC 1408
Db 1485 GCTGATTGCTGCATTAAGCCACGATTTGGATCAGCGTGTGTGAATACTCTTTACATACA 1544
QY 1409 TAAGATGGCTCTGCTCCCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCACA 1468
Db 1545 GCGAAGTGAACATCCACTTGGCCAGCTTTACTG---CCATTCATCATGGAACACATCA 1601
QY 1469 TTTCAACCAACCGGATGATGCTTCAAGTGAAGGTGCACATATCTTTTGTAACTGTC 1528
Db 1602 TTTTGACCACTGCTGATGATTTCTTAATAGTCCAGCAATCAGATCTCAGTGGCTCTC 1661
QY 1529 CTCCAAGAAATATAGTGACCTTATGACCTTTTGAAGCAGTCAATATTTGGCAACAGCT 1588
Db 1662 CATTGAAGAAATATAGACCACTGTTGAANAATATCAAGCAAGCTATTTTAGCTACAGCT 1721
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Db	1411	TTTGCCAACTGTTTAATAGATGGAGGAGATACTGGC--AAGTTAAGCCTTTCAACGG	1468
QY	881	TGCAGATCAACAGCATTGTTAGGCTTTTGTGCTATCTTTGTGACATTGGCATCAACAAC	940
Db	1469	AAATGACGAACAGTTTCTGGAGCTTTTGTCTATCTTTGTGGCTTGGGATCCACAAC	1528
QY	941	AATATGATGATCAAGTGAAGAAGTCTGGGCCAAGCAGTCTGGGCTCTTTGATGTGCT	1000
Db	1529	GCAGATGATGAAGCAGTGGAGAGCCATGGCCAAGCAAAATGGTCACATTGGAGGTTCT	1588
QY	1001	ATCATACCATCAACATGTTCAAAAGCTCAAGTTGACRAGTTTAAGGCAGCCAAACATCCC	1060
Db	1589	GTGCTATCATGCTTCAGCAGCAGAGGAAGAAACAAGAGAGCTACAGCTGTAGCGGCTGC	1648
QY	1061	TCGTGTGTCA-----GAACTTGGCCATCGATGACATTCATTTTGTGACTTTCTCT	1111
Db	1649	TGTGTGCTATCTGCCAGACCCTTAAATTTACTGCTTTAGCTTTCAGTGACCTTGAGCT	1708
QY	1112	CGACCTTGATGCCATGATCAGCTGCTCTCGGATGTTTCATPGAGCTGGGATGGTACA	1171
Db	1709	GTCTGATCTGGAACAGCAGCTGTGTACAATTCGGATGTTTACTGACCTCAACCTTGTGCA	1768
QY	1172	GAAATTTAAATTTGACTATGACACACTGTGTAGTGGCTTTTCACAGTCAGGAAAAACTA	1231
Db	1769	GAACTTCCAGATGAACATGAGGTTCTTTCAGATGGATTTTAAAGTTTAAGAAGAAATTA	1828
QY	1232	TCGGATG---GTTCTATACCAACATGGAGACATGCTTCAACGTGTGTACGCTGATGTT	1288
Db	1829	TCGGAAGATGTTGGCTATCATAAATTTGAGACATGCCCTTAAATACAGCTCAGTGTGAT	1888
QY	1289	CGCGATGTTAACCATGCTGTGGTCTTCAAGACATTCGACCGAGGTGGAAATTTTAGCGGT	1348
Db	1889	TGCTGCTCTAAAAGCAGGCAAAATTCAGAAACAGCTGACTGACCTGGAGATACTTGCATT	1948
QY	1349	GATTTGGGATGCCGTGTCTATGACCTCGACCACAGGGGAACCAACATGCCCTTCCAAGC	1408
Db	1949	GCTGATGTGTCACTAAGCCACGATTTGGATCACCCTGGTGTGAATACTCTTACATACA	2008
QY	1409	TAAGATGTGCTGTGCCCTGGCCAACTCTATGAACTCTGTAGCTTGGAGCATCACCA	1468
Db	2009	CGGAAGTGAACATCCACTTGCCCGAGCTTTACTG---CCATTCAATCATGGAACACATCA	2065
QY	1469	TTTCAACACGCGGTGATGATCCTTCAAGTGAAGGTACAAATATCTTTGTCAACCTGTC	1528
Db	2065	TTTTCACCAAGTGCCTGATGATTTCTTAATAGTCCAGCAATCAGATTCTCAGTGGCTCTC	2125
QY	1529	CTCCAAGGAATATAGTACCTTTATGACCTTTTGAAGCATCAATATTGGCAACACACT	1588
Db	2126	CATTGAAGAAATATAGACCACGTTGAAAATAATCAAGCAAGCTATTTTAGCTACAGACT	2185
QY	1589	CACGCTGTACTTTGAGAGAGAACTGAATTTCTTGAACCTTGTCAAGTAAAGGAGATACGA	1648
Db	2186	AGCACTGTACATTAGAGCGGAGGAGAAATTTTGAACCTTATAAGAAAAATCAATCAA	2245
QY	1649	TTGGAACATCAAAAACCATGCTGATATTTTCGATCAATGTTTAAATGACAGCCTGTGACCT	1708
Db	2246	TTTGGAAAGATCTCATCAAAAGGAGTTGTTTGGCAATGCTGATGACAGCTTGTGATCT	2305
QY	1709	TGGAGCCGTGACCAACCCGTGGAGATCTCCAGACAGGTGGGAGACTTGTAAACAGTGA	1768
Db	2306	TTCTGCAATTTACAAAACCCGTGCCCTATTCAACACGGATAGCAGAACTTGTAGCAACTGA	2365
QY	1769	GTCTTTCGAAACAGGAGATCGGAGAGATTAGAGCTCAAACTCACTCCCTTCAGCAATTTT	1828
Db	2366	ATTTTTTGTATCAAGGAGCAGAGAGAGAAAGAACTCAACATAGAACCCACTGATCTAAT	2425
QY	1829	TGATCGGAACCGGAAGGATGAATGCCCTCGTTCGAACTGGAGTGGATTGATAGCATCTG	1888
Db	2426	GAACAGGGAGAGAAAAACAAATCCCAAGTATGCAAGTTGGGTTTCATAGATGCCATCTG	2485
QY	1889	CATGCCCTTGTATCAGGCTGCTGAAGTCAACGTGAACCTGAACCCCATGCTAGATTC	1948
Db	2486	CTTGCAACTGTATGAGGCCCTTGACCACGCTGCAGAGGACTGTTTCCCTTTGCTAGATGG	2545

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